

FIG. 1A

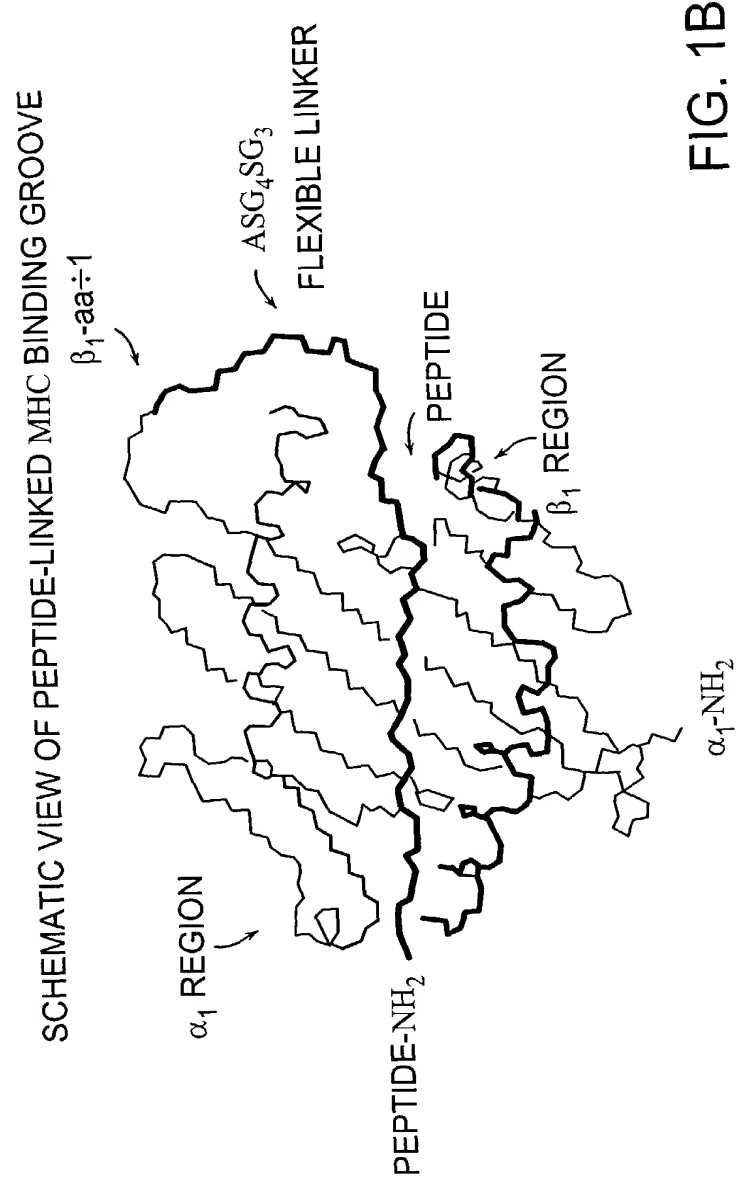


FIG. 1B

SCHEMATIC VIEW OF SOLUBLE PEPTIDE-LINKED MHC-IgG C-REGION FUSION PROTEIN

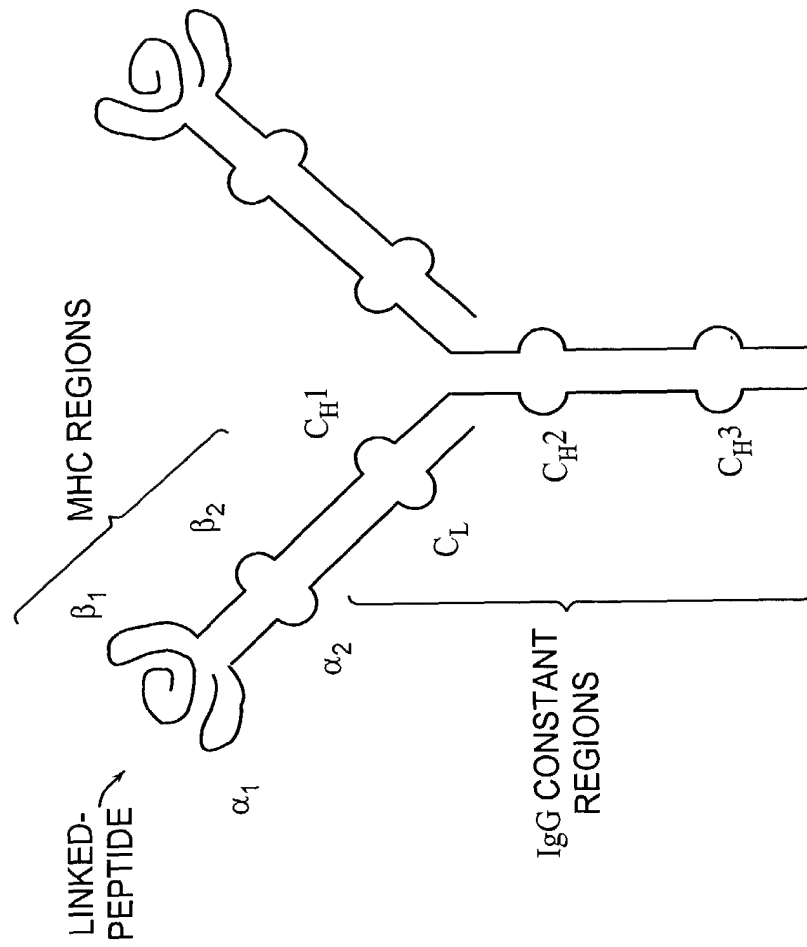


FIG. 1C

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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I-A^d α CHAIN CLONING SCHEME

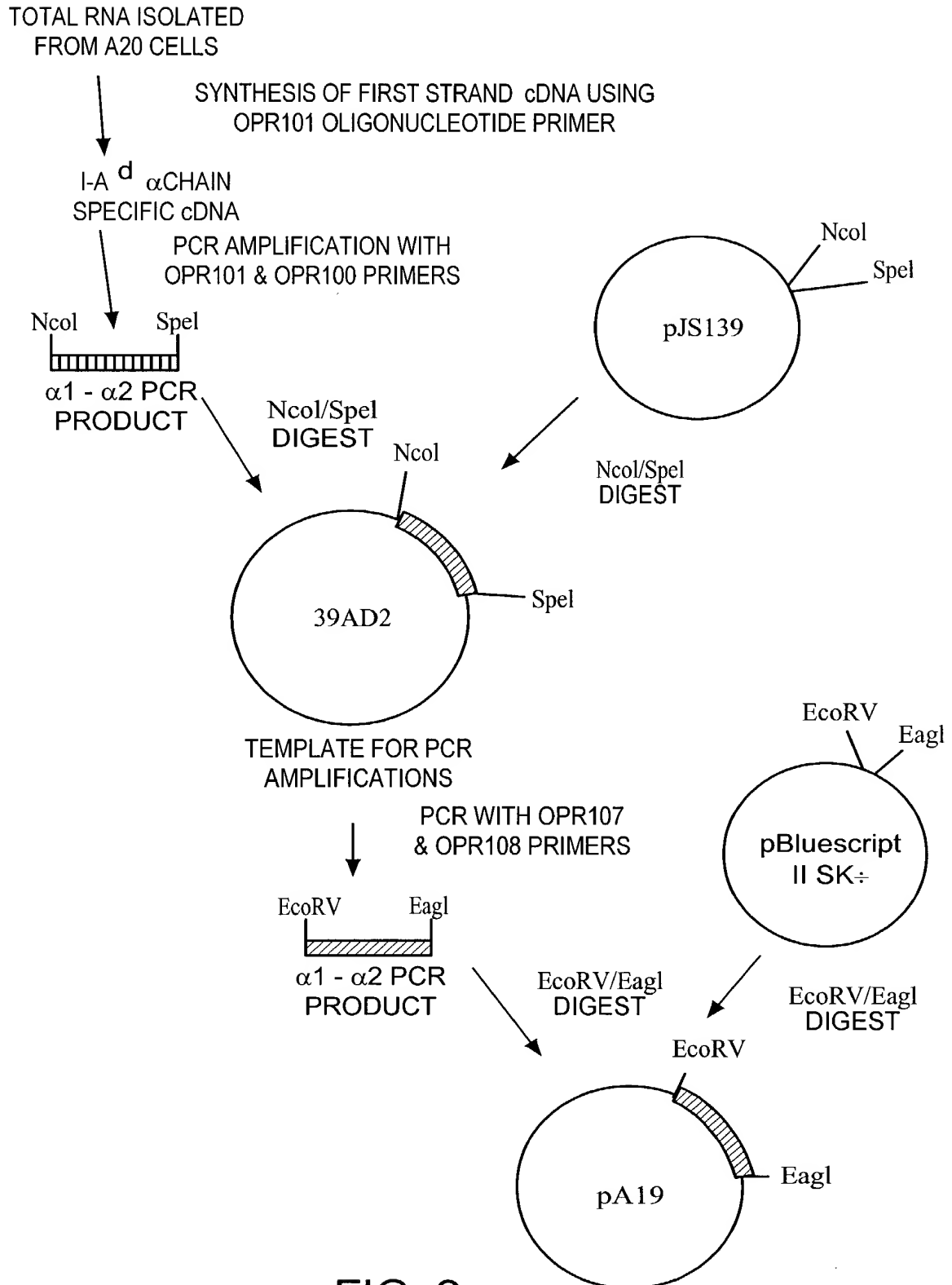
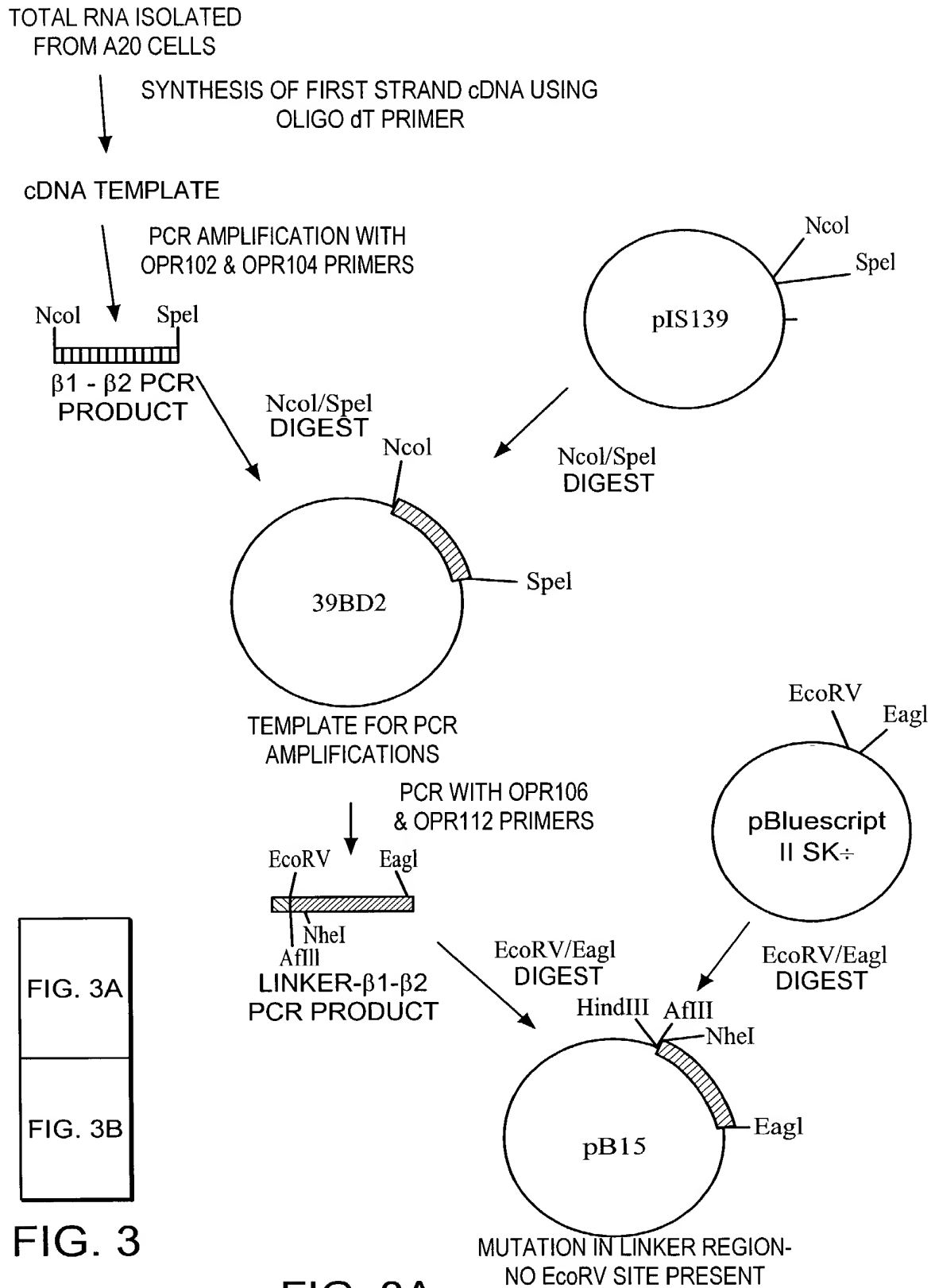


FIG. 2

I-A^d β CHAIN CLONING SCHEME

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Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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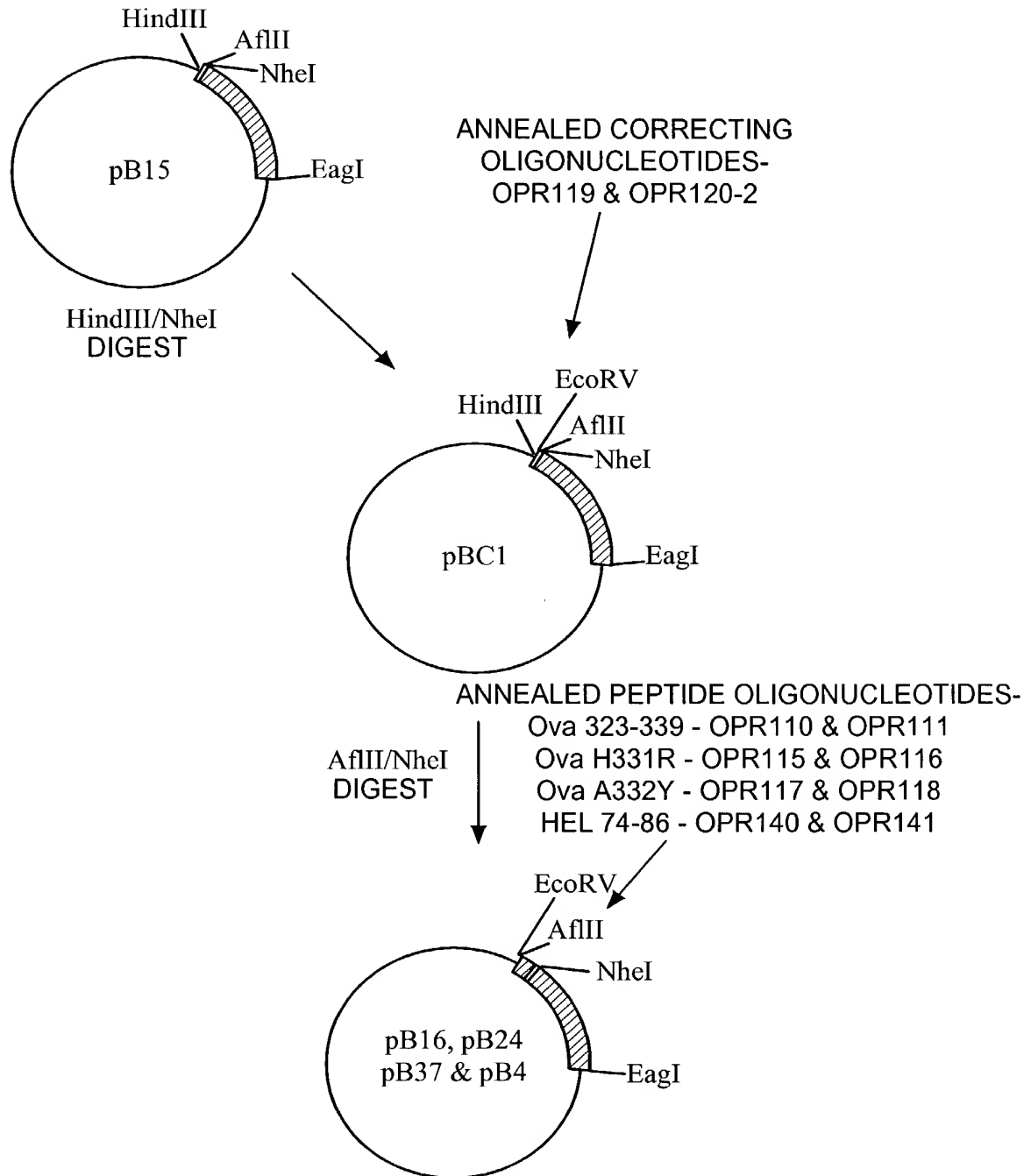
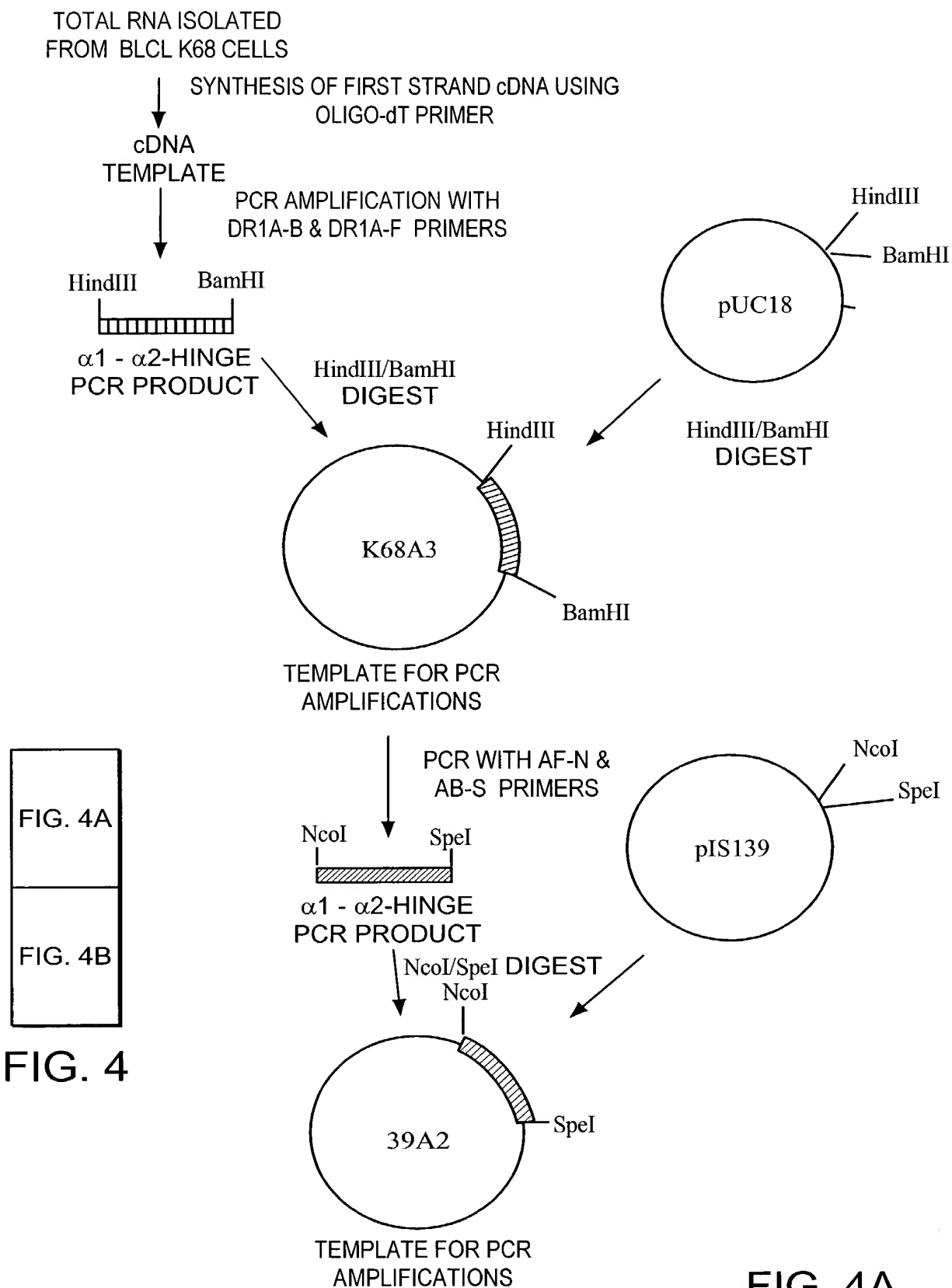


FIG. 3B

HLA-DRI α CHAIN CLONING SCHEME

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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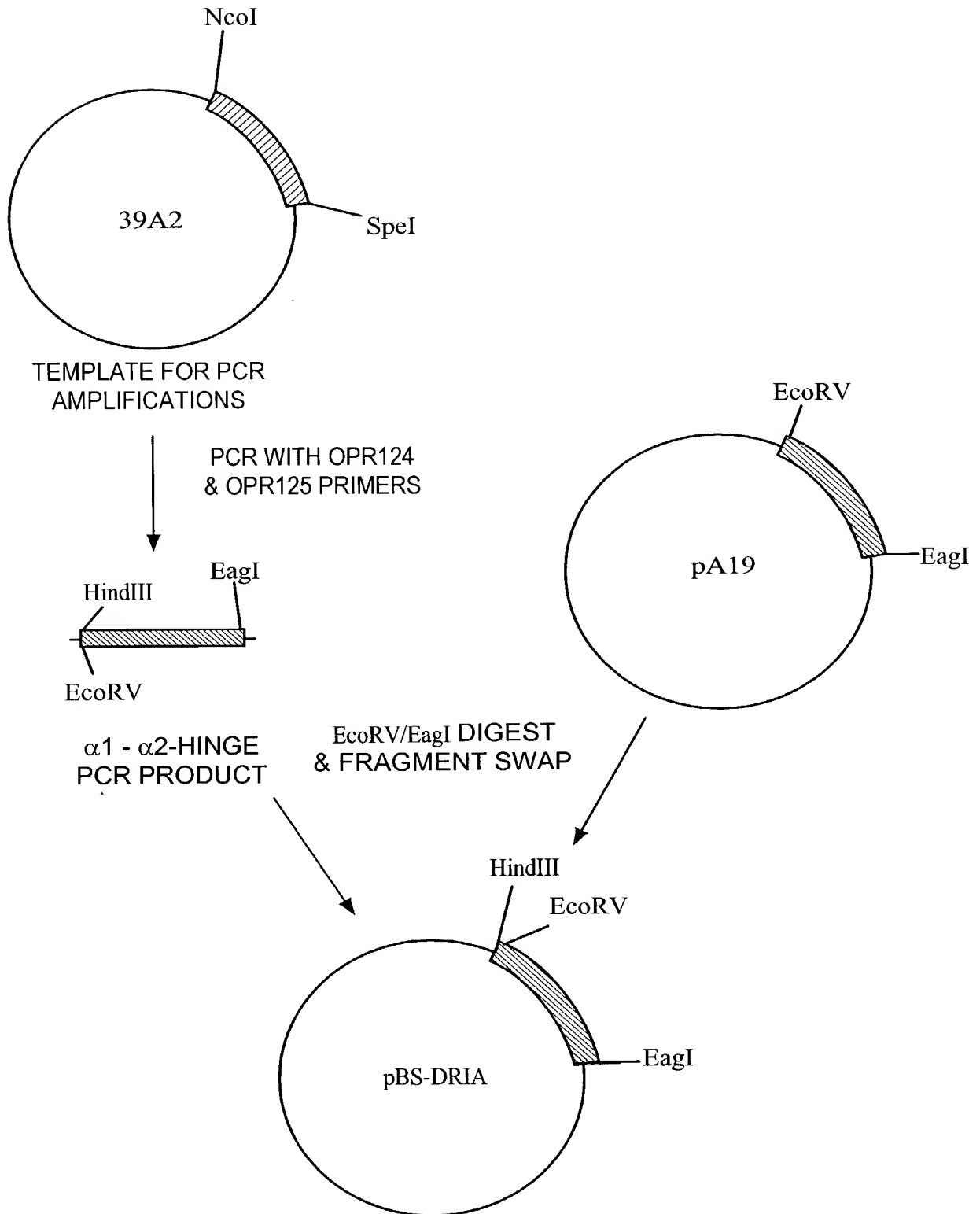
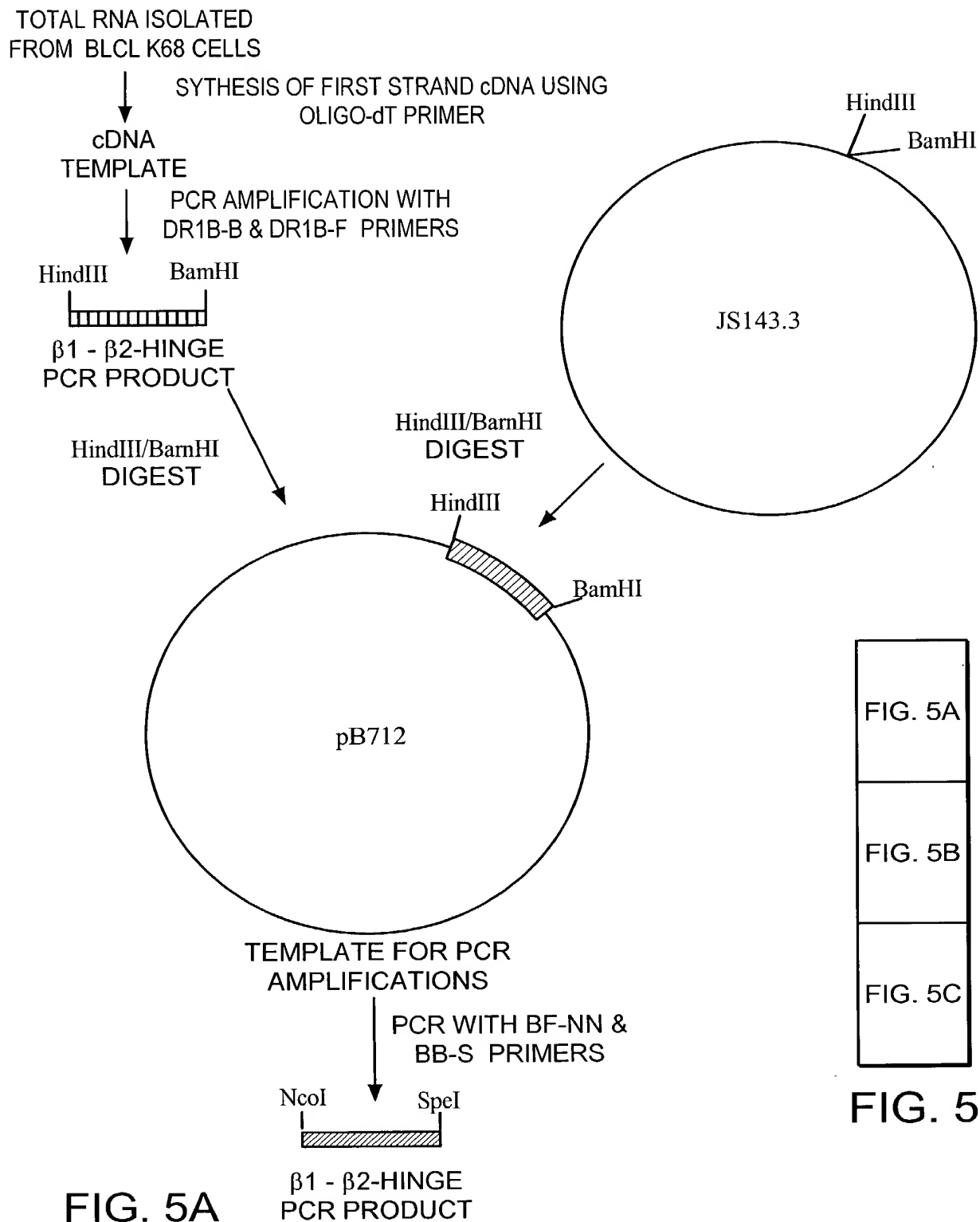


FIG. 4B

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HLA-DRI β CHAIN CLONING SCHEME



Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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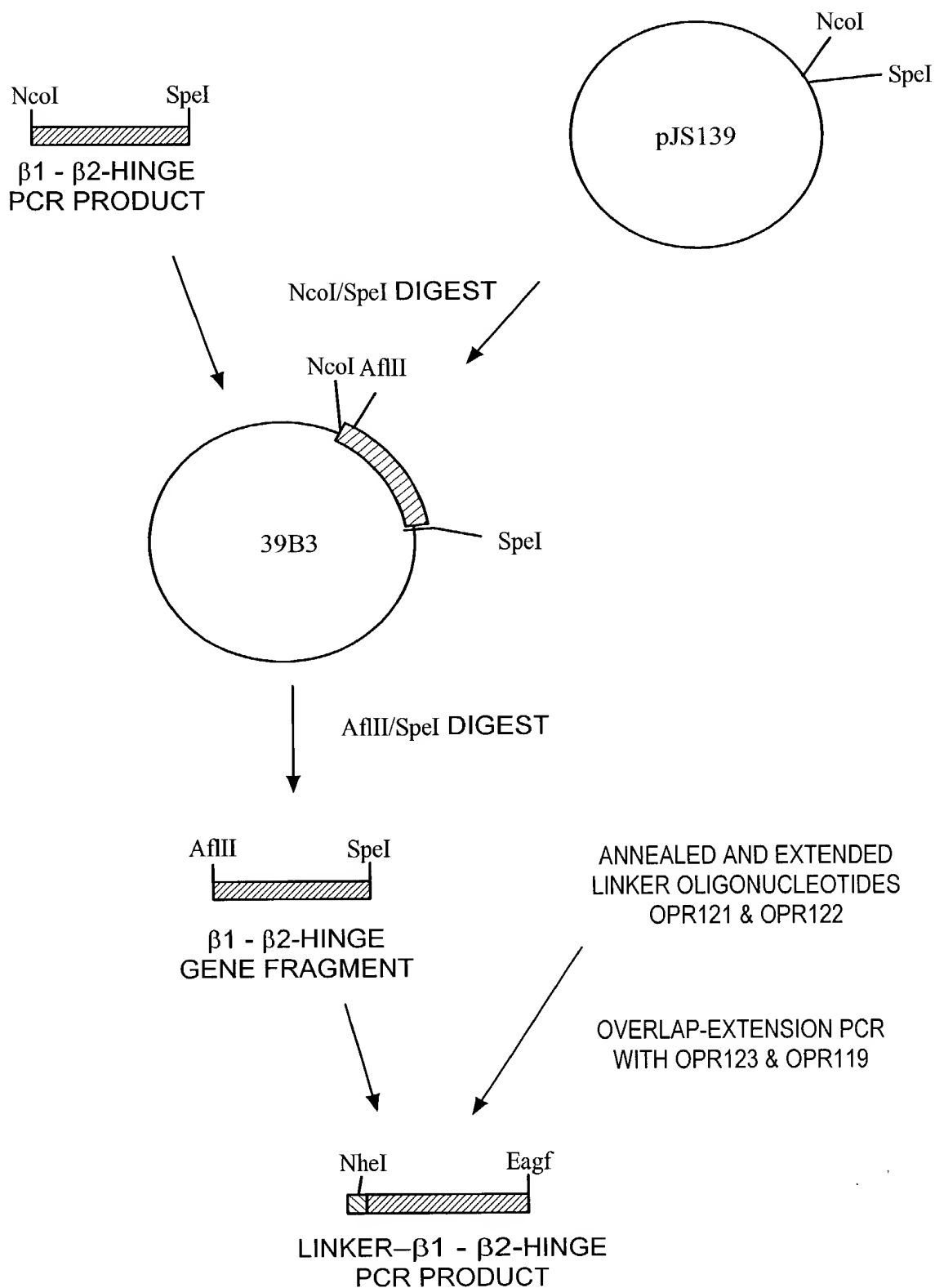


FIG. 5B

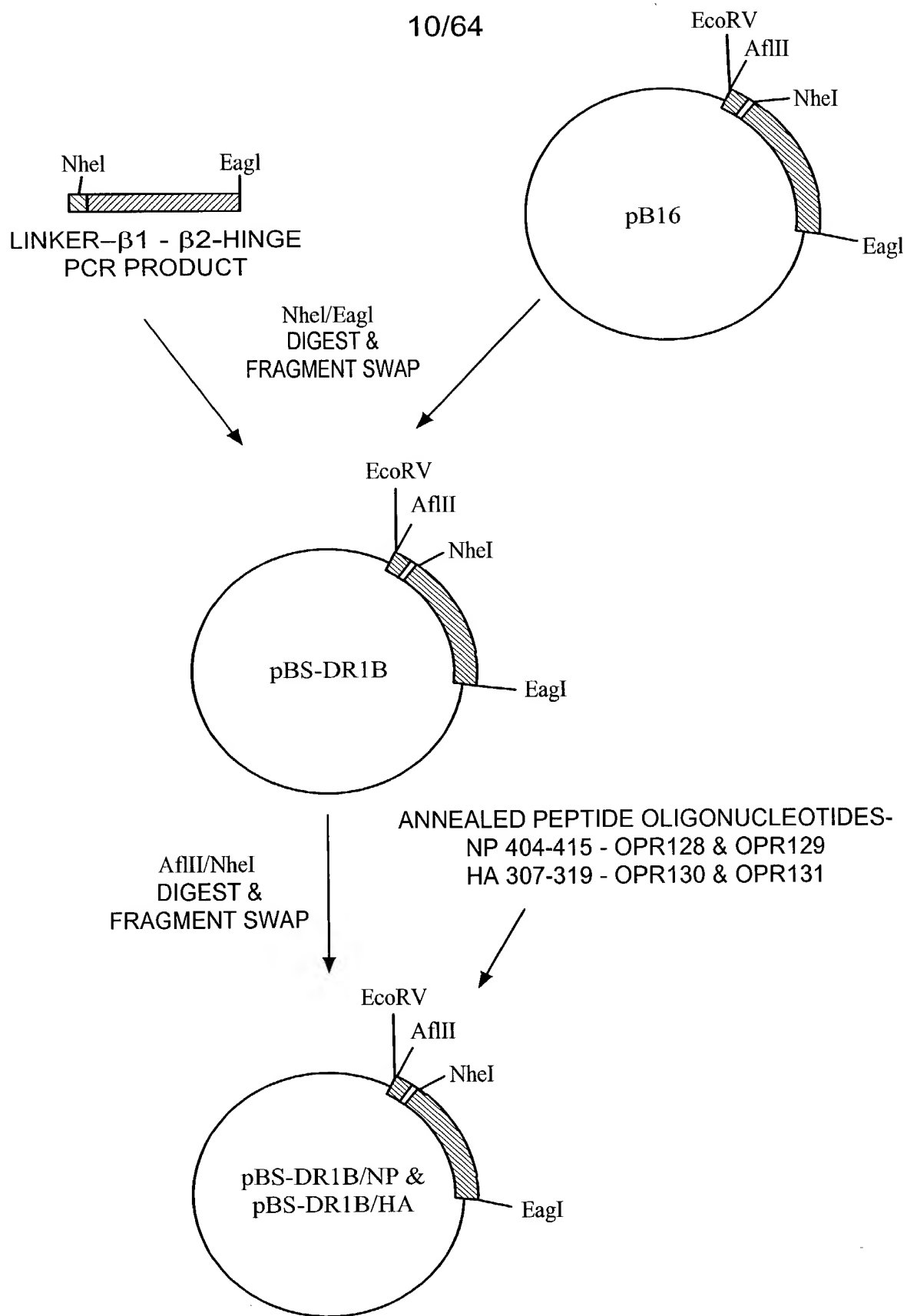


FIG. 5C

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

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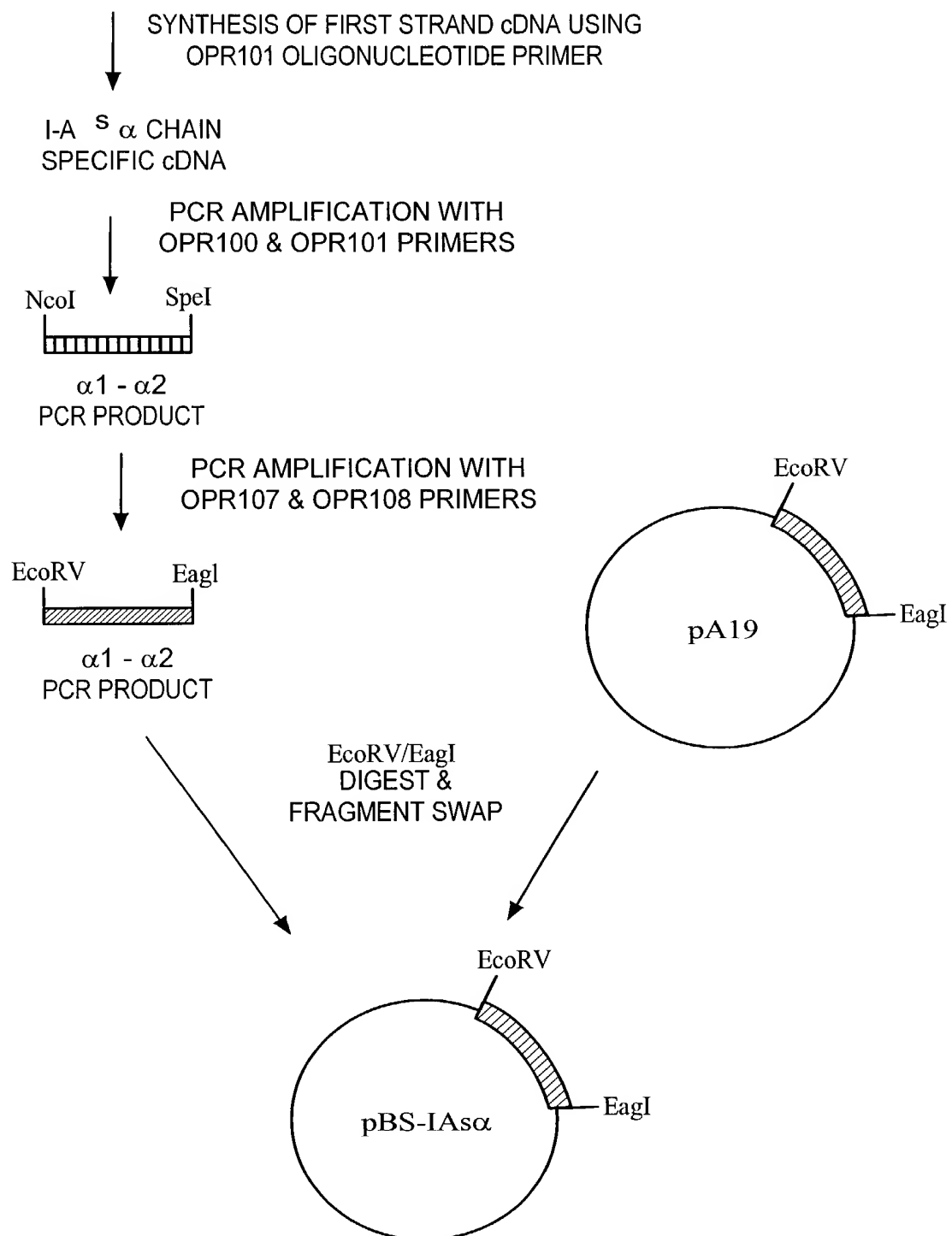
I-A^S α CHAIN CLONING SCHEMETOTAL RNA ISOLATED FROM
SJL MOUSE SPLEEN CELLS

FIG. 6

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I-A^S β CHAIN CLONING SCHEME

TOTAL RNA ISOLATED FROM
 SJL MOUSE SPLEEN CELLS

↓ SYNTHESIS OF FIRST STRAND cDNA USING
 OPR106 PRIMER

I-A^S β CSPECIFIC
 cDNA TEMPLATE

↓ PCR AMPLIFICATION WITH
 VW310 & OPR106 PRIMERS

β1 - β2
 PCR PRODUCT

↓ PCR AMPLIFICATION WITH
 VW309 & OPR106 PRIMERS

NheI EagI
 LINKER-
 β1 - β2
 PCR PRODUCT

NheI/EagI
 DIGEST &
 FRAGMENT SWAP

pBS-IAsβ

pB16

ANNEALED PEPTIDE OLIGONUCLEOTIDES-
 MBP 91-103 - VW315 & VW316
 PLP 139-151 - VW313 & VW314
 MBP 1-14 - VW317 & VW318

AflII/NheI
 DIGEST &
 FRAGMENT SWAP

pBS-IAsβ/MBP91,
 pBS-IAsβ/PLP &
 pBS-IAsβ/MBPI

FIG. 7

FIG. 8A

FIG. 8B

FIG. 8C

FIG. 8D

FIG. 8

OLIGOMICLEOTIDES USED IN CONSTRUCTING MHC VECTORS

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I-A^d/I-A^s PCR PRIMERS AND CLONING OLIGENUCLEOTIDES
(RESTRICTION SITES ARE UNDERLINED)

OPR100

5'-GGG GGG GCC ATG GCC GAA GAC GAC ATT GAG GCC GAC-3'

OPR101

5'-GGG GGG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107

5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG
GCC G-3'

OPR108

5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG
C-3'

OPR102

5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104

5'-GCG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106

5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112

5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119

5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'

OPR120-2

5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310

5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309

5'-CGA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136

5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

FIG. 8A

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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OPR132

5'-CCC CCC AAG CTT CCC GGG CGA CCA TGG CTC TGC AGA TCC CCA
 GC-3'

OPR133

5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

HLA-DR1 PCR PRIMERS AND CLONING OLIGONUCLEOTIDES

DR1A-F

5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DR1A-B

5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DR1B-F

5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG
 CAG C-3'

AF-N

5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S

5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124

5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA
 GAA GAA CAT GTG ATC-3'

OPR125

5'-GGG GGG CGG CCG CTA CTT ACG TTT CTC TGG GAG AGG GCT TGG
 AGC-3'

DR1B-B

5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN

5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA
 CGT TTC TTG-3'

BB-5

5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

FIG. 8B

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OPR121

5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT
GGT GGG GAC ACC CG-3'

OPR122

5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG
GGT GTC CCC ACC ACC-3'

OPR123

5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-
3'

PEPTIDE OLIGONUCLEOTIDES.

Ova 323-339

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

HEL 74-86

OPR140

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC
TCC G-3'

OPR141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAGBGGG ATG TTG CAC AGG
TTA C-3'

FIG. 8C

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
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NP 404-415

OPR129

5' - TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G - 3'

OPR129

5' - CTA GCC TGC ACG CTG AAG GCG GGC TEA ACG CTG ATC TGA C - 3'

HA 307-319

OPR130

5' - TTA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC
ACC G - 3'

OPR131

5' - CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG
GGA C - 3'

MBP 91-103

VW315

5' - TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG
CGC G - 3'

VW316

5' - CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG
TGA C - 3'

PLP 139-151

VW313

5' - TTA CAC CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG
TTC G - 3'

VW314

5' - CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG
TGA C - 3'

MBP 1-14

VW317

5' - TTA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG
TAC CTG G - 3'

VW316

5' - CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT
GCC ATA C - 3'

FIG. 8D

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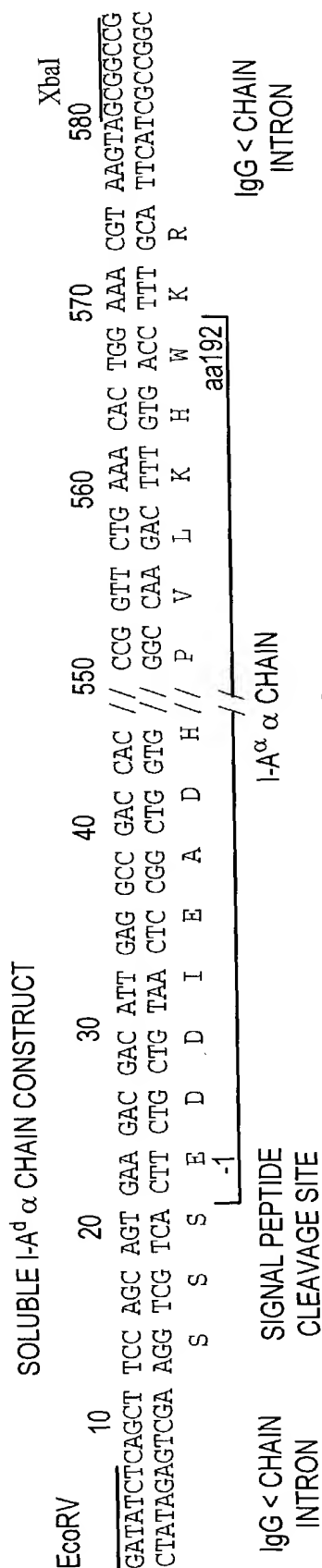


FIG. 9A

SOLUBLE I-A^d β CHAIN CONSTRUCT

RESTRICTION SITES FOR INSERTION OF
 OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

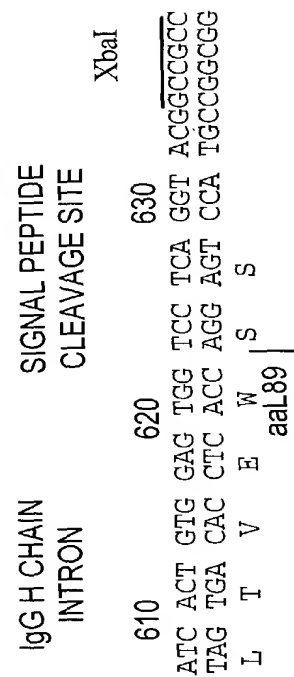
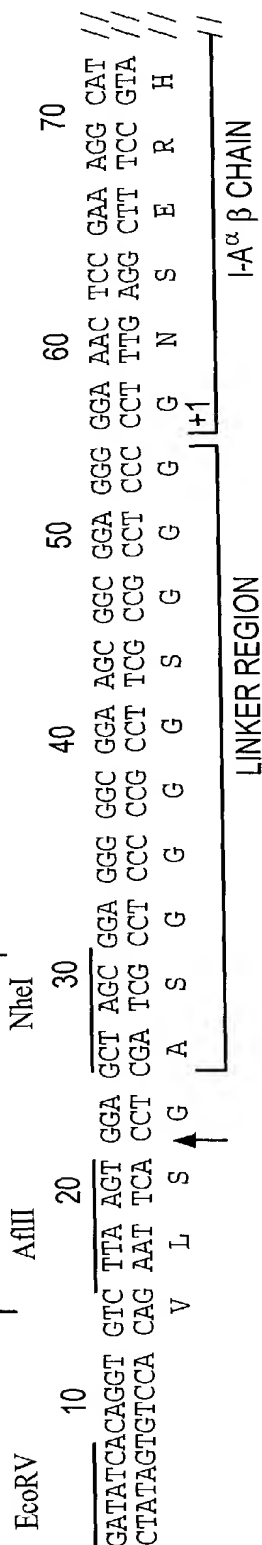


FIG. 9B

SOLUBLE I-A^d β CHAIN CONSTRUCT

RESTRICTION SITES FOR INSERTION OF
 OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



SOLUBLE I-A^d α CHAIN CONSTRUCT

RESTRICTION SITES FOR INSERTION OF
 OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST



Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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SOLUBLE I-A^s α CHAIN CONSTRUCT

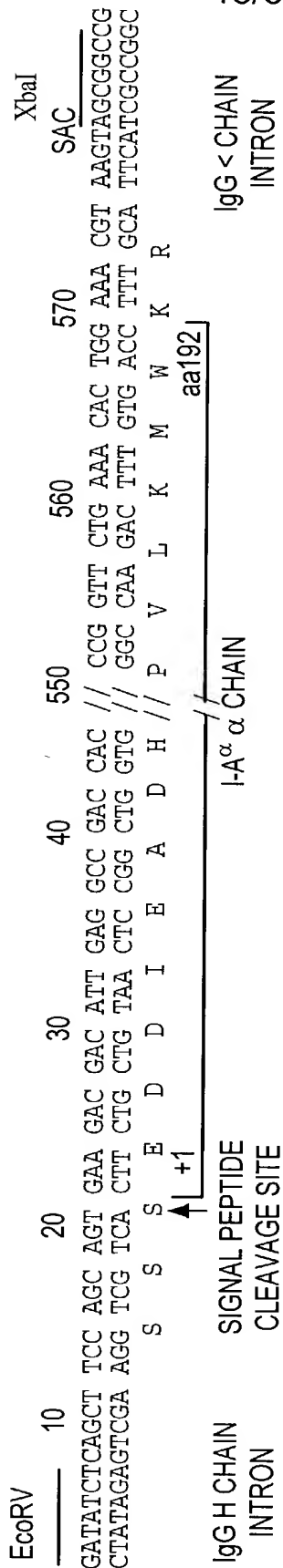


FIG. 9C

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

FIG. 9D

SOLUBLE HLA-DR1 α CHAIN CONSTRUCT

[illegible]

FIG. 9E

SOLUBLE HLA-DRI β CHAIN CONSTRUCT

RESTRICTION SITES FOR INSERTION OF OLIGONUCLEOTIDES ENCODING PEPTIDES OF INTEREST

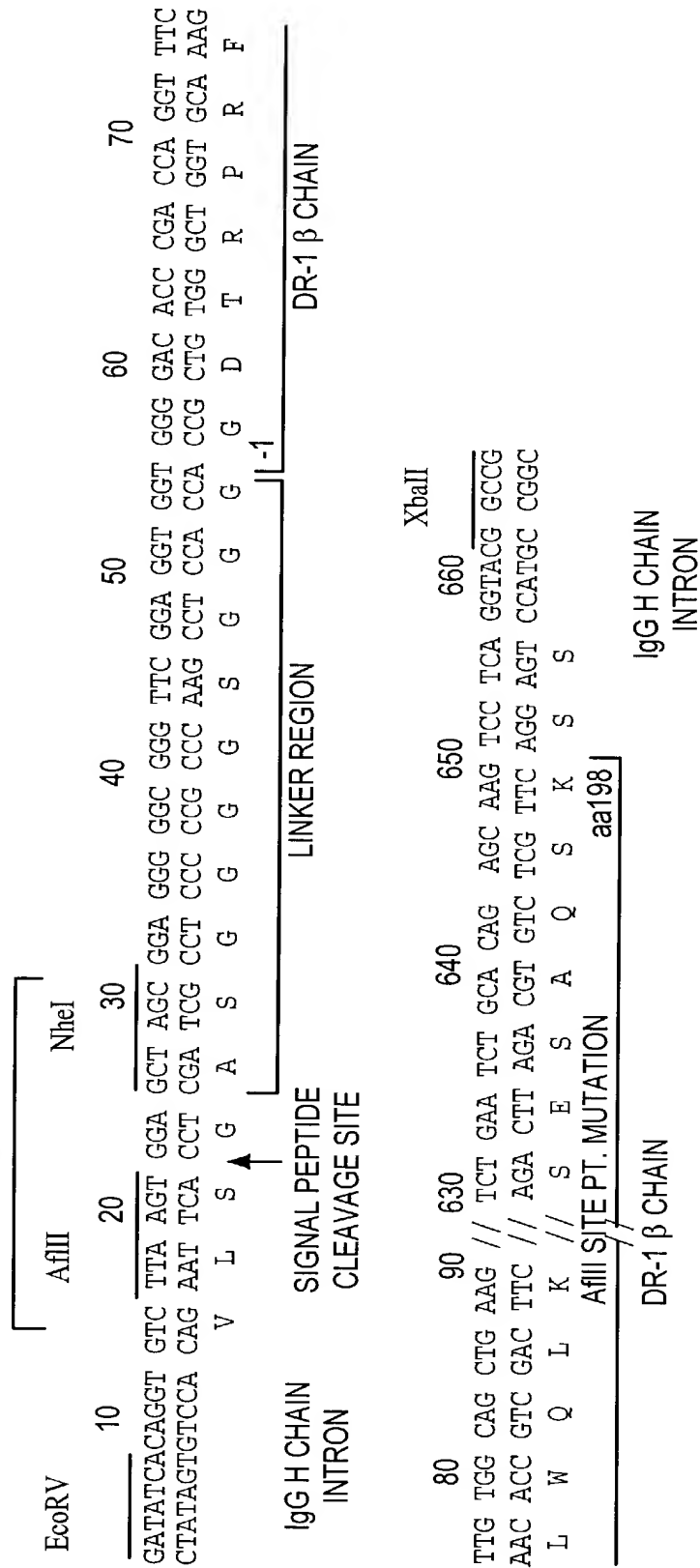


FIG. 9F

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

USSN 09/900,379

ORIGINAL MAMMALIAN CELL EXPRESSION VECTORS

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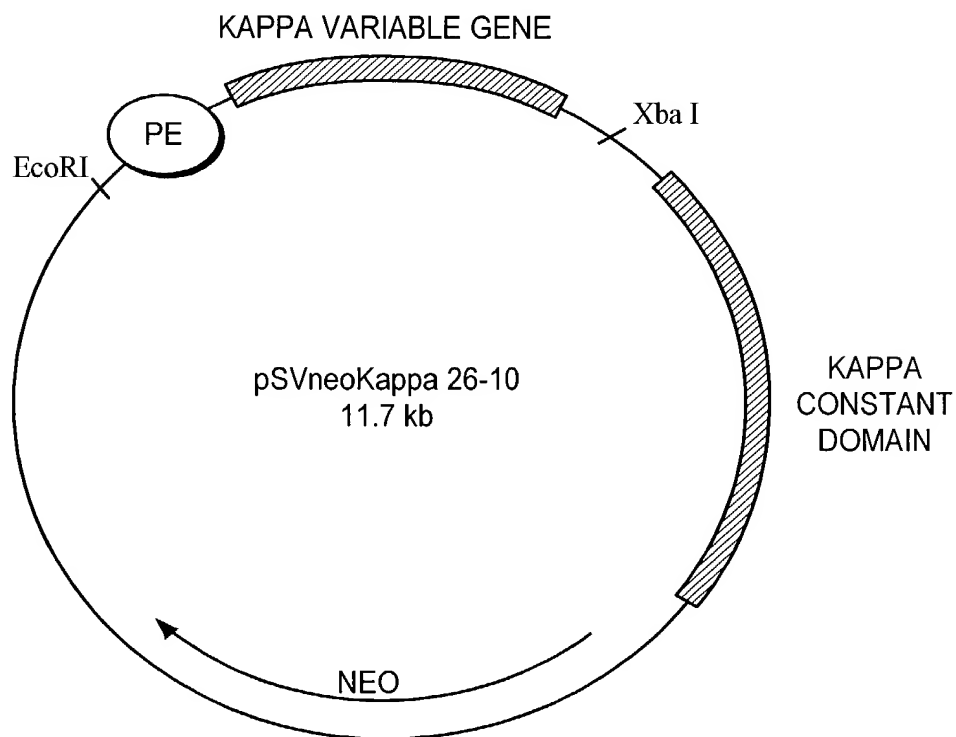


FIG. 10A

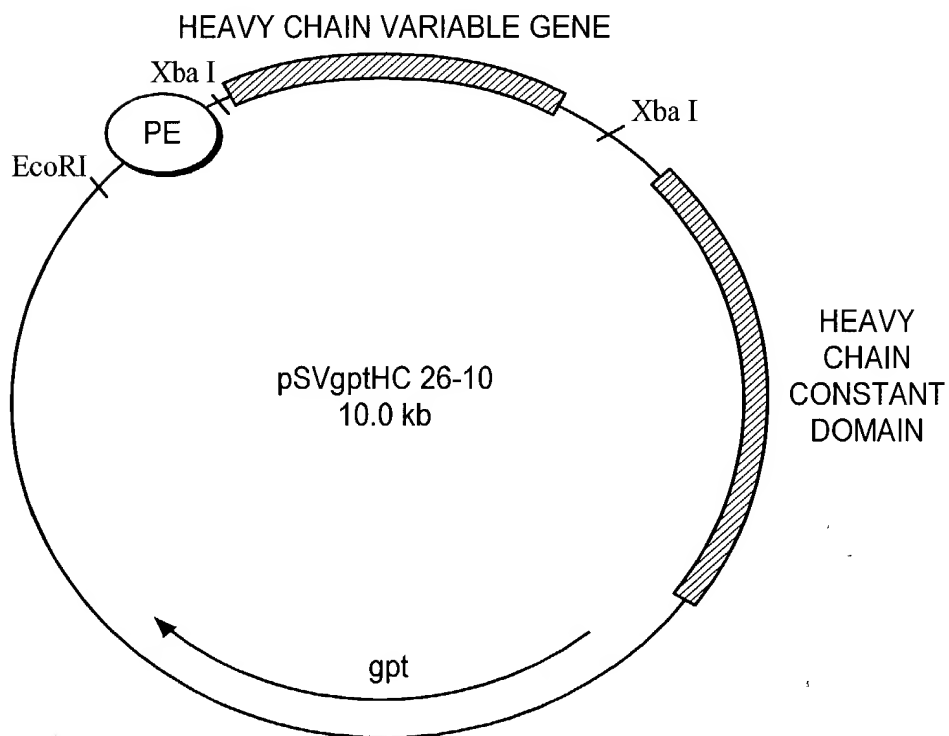


FIG. 10B

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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THE 2.7 Kb KAPPA AND THE 1.7 Kb HEAVY CHAIN EcoR V AND Eag I. MUTATED CONSTRUCTS

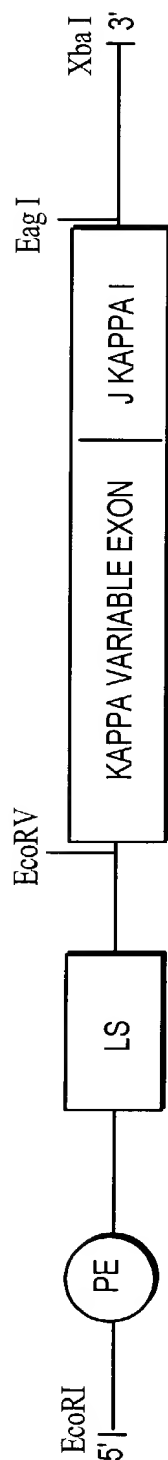


FIG. 11A



FIG. 11B

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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PCR SITE DIRECTED MUTAGENESIS FOR INTRODUCING EcoRV and EagI
 RESTRICTION SITES INTO KAPPA CHAIN 2.7 kb INSERT

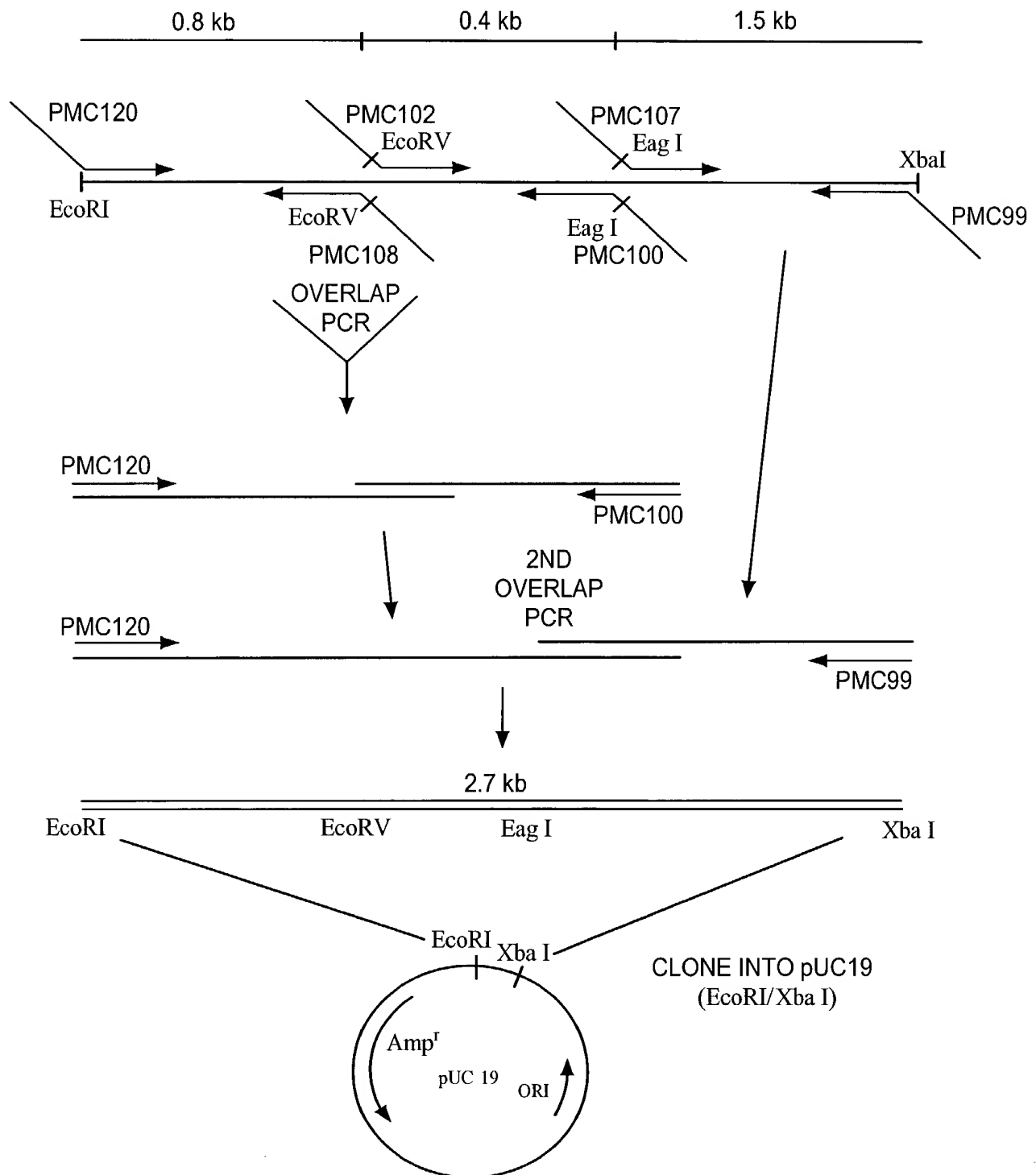


FIG. 12

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STRATEGY FOR CONSTRUCTING MHC CLASS II α /KAPPA CONSTANT
 GENE IN MAMMALIAN CELL EXPRESSION VECTOR

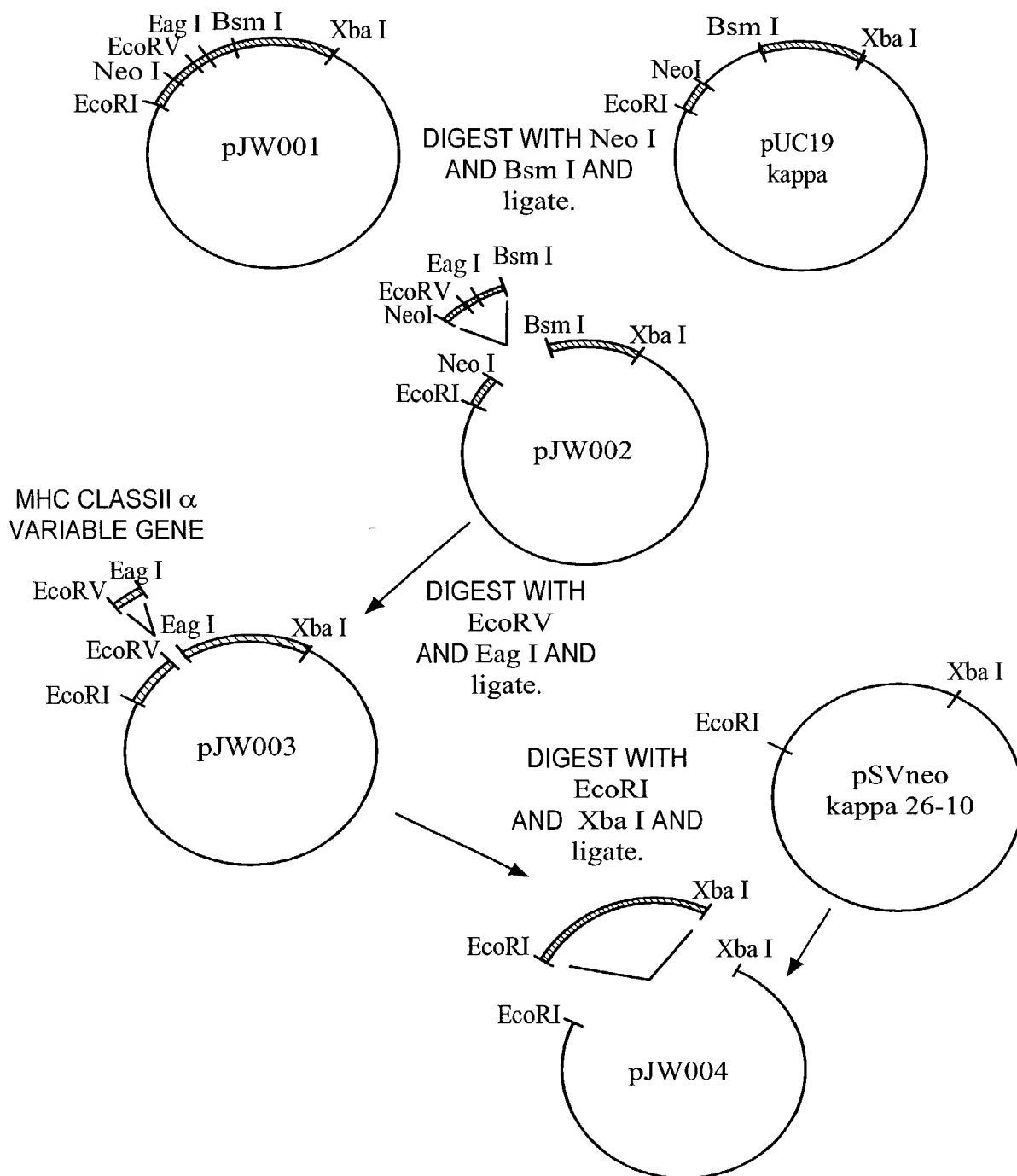


FIG. 13

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

PRIMERS USED FOR SEQUENCING MUTATED 2.7Kb FRAGMENT

<u>PRIMER LIST</u>	<u>SEQUENCE</u>
PMC-33	(5 ' GCTCAGCTGTCTTGTTCAGTACTGATC3 ')
PMC-77	(5 ' GTAAGTAGCGGCCG3 ')
PMC-111	(5 ' GGTATGTAAAAATAAACATCACAG3 ')
PMC-114	(5 ' GCTTTGCTTACGGAGTTACTC3 ')

FIG. 14

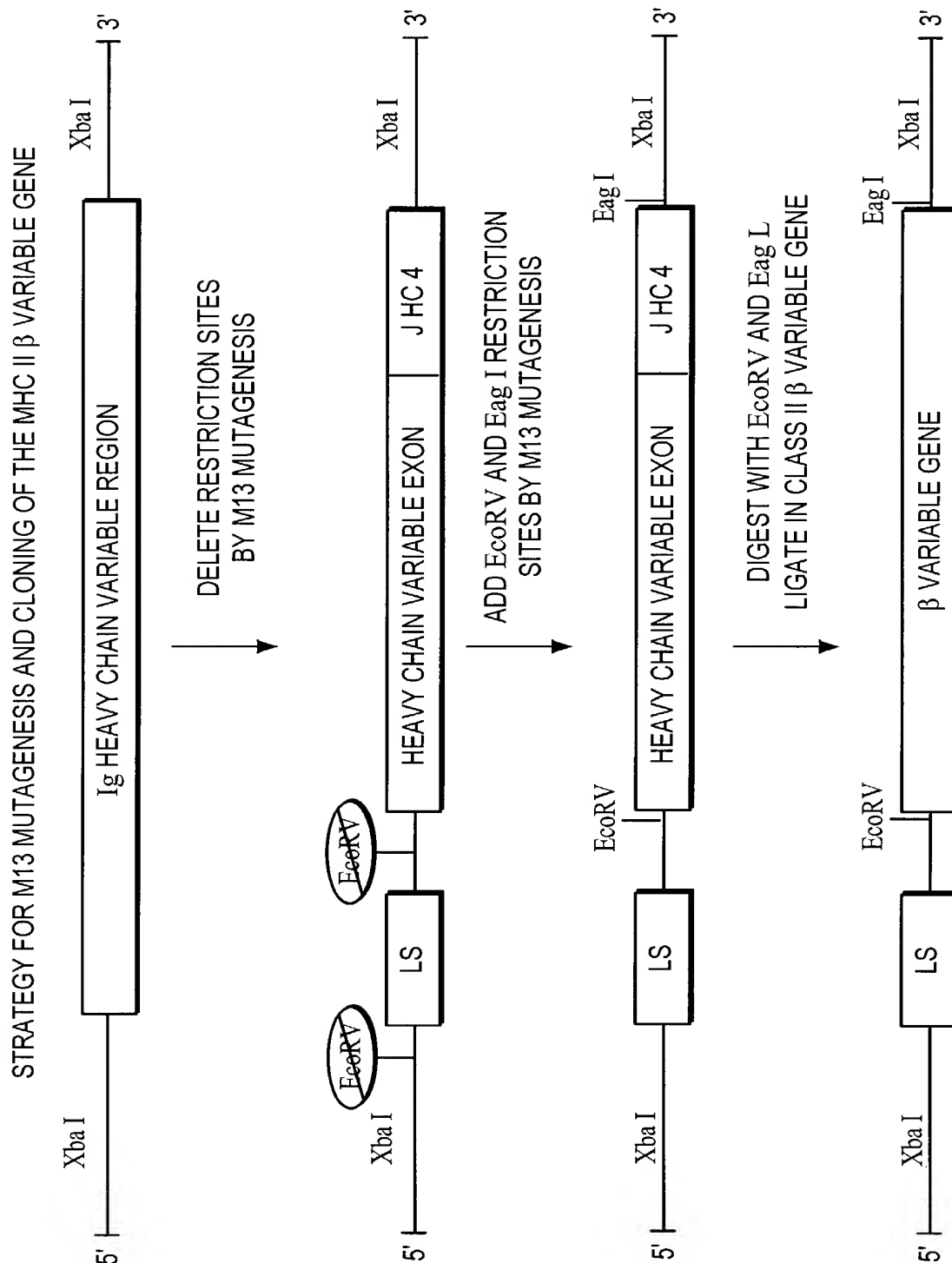


FIG. 15

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

USSN 09/900,379

FINAL VECTORS FOR EXPRESSING MHC II/Ig CHIMERIC PROTEINS 27/64

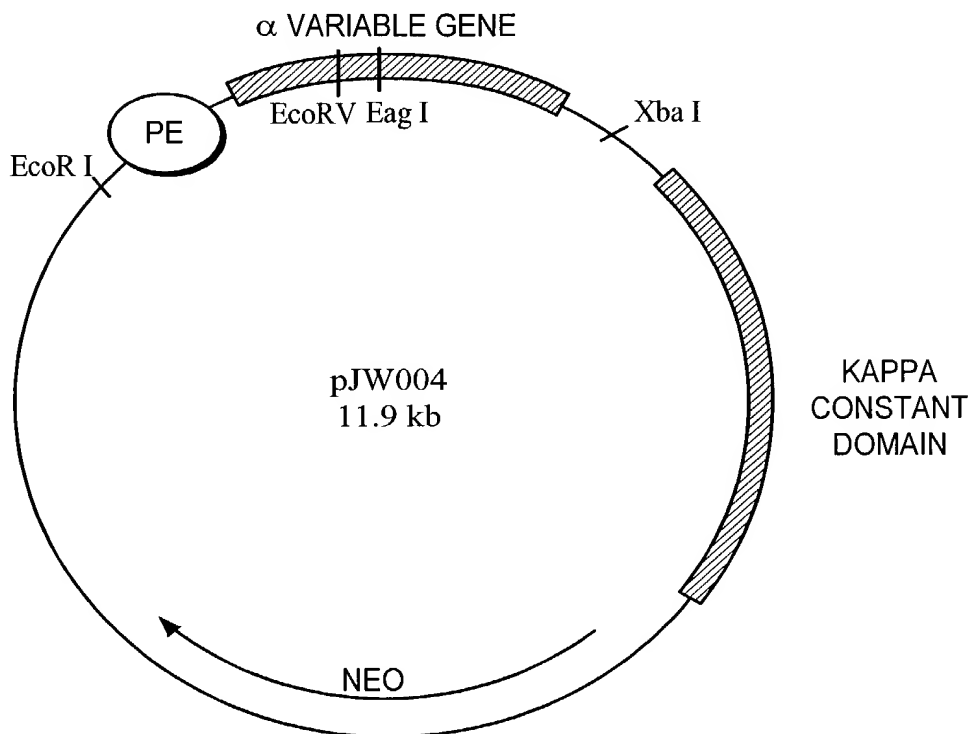


FIG. 16A

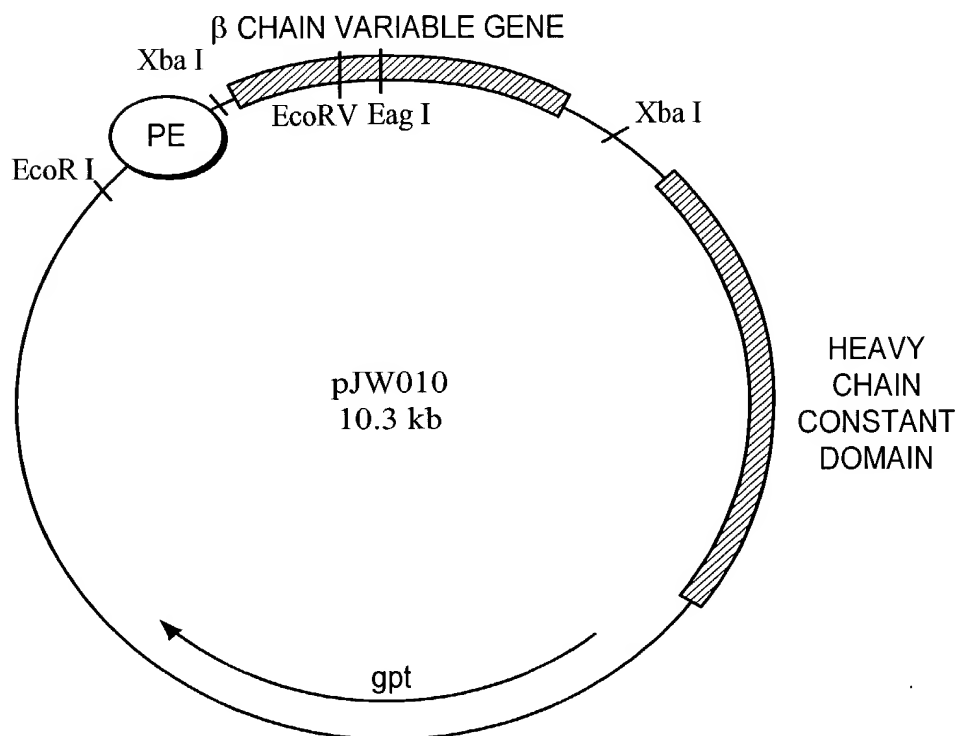


FIG. 16B

FIG. 17A

FIG. 17B

FIG. 17C

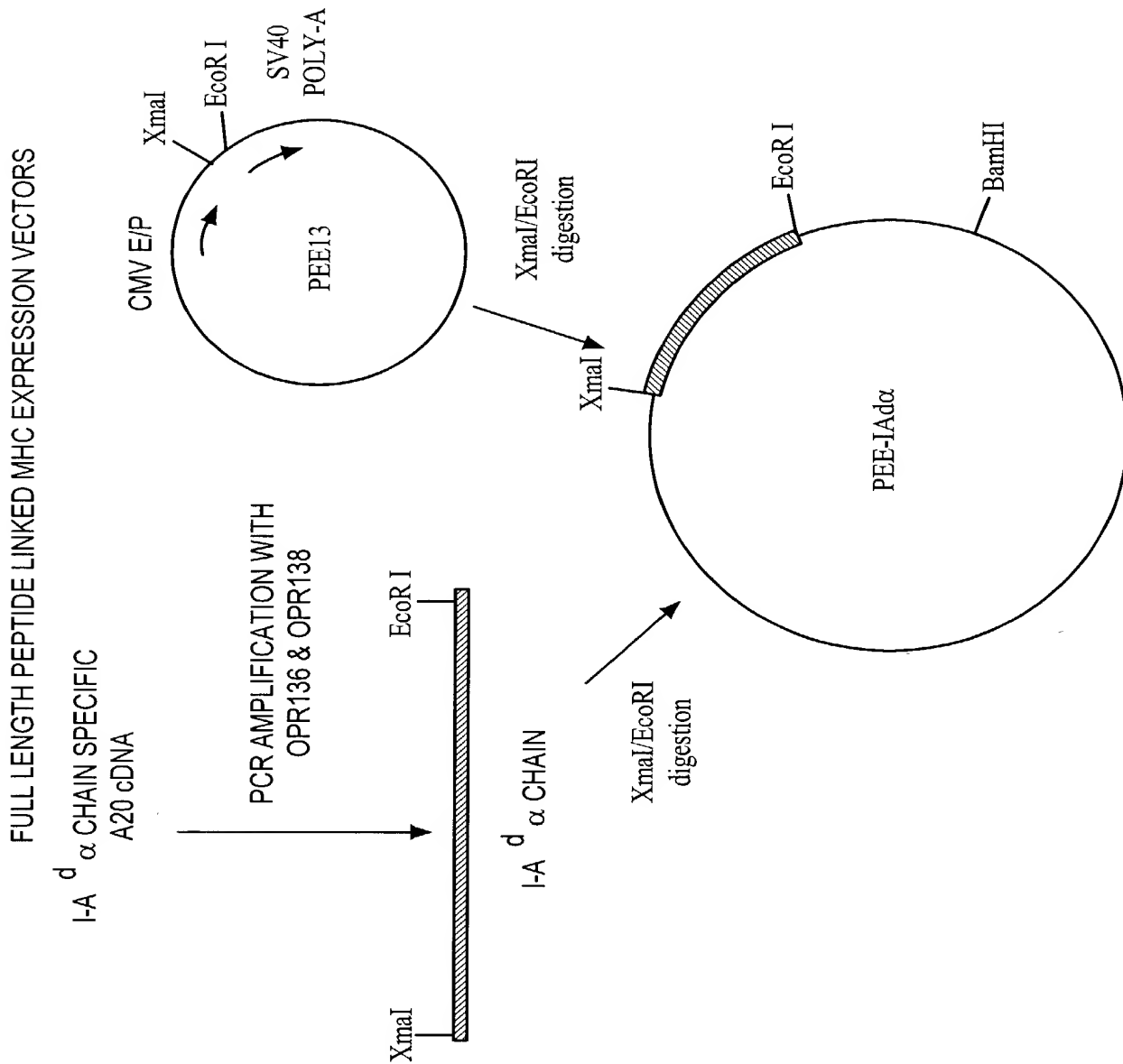


FIG. 17A

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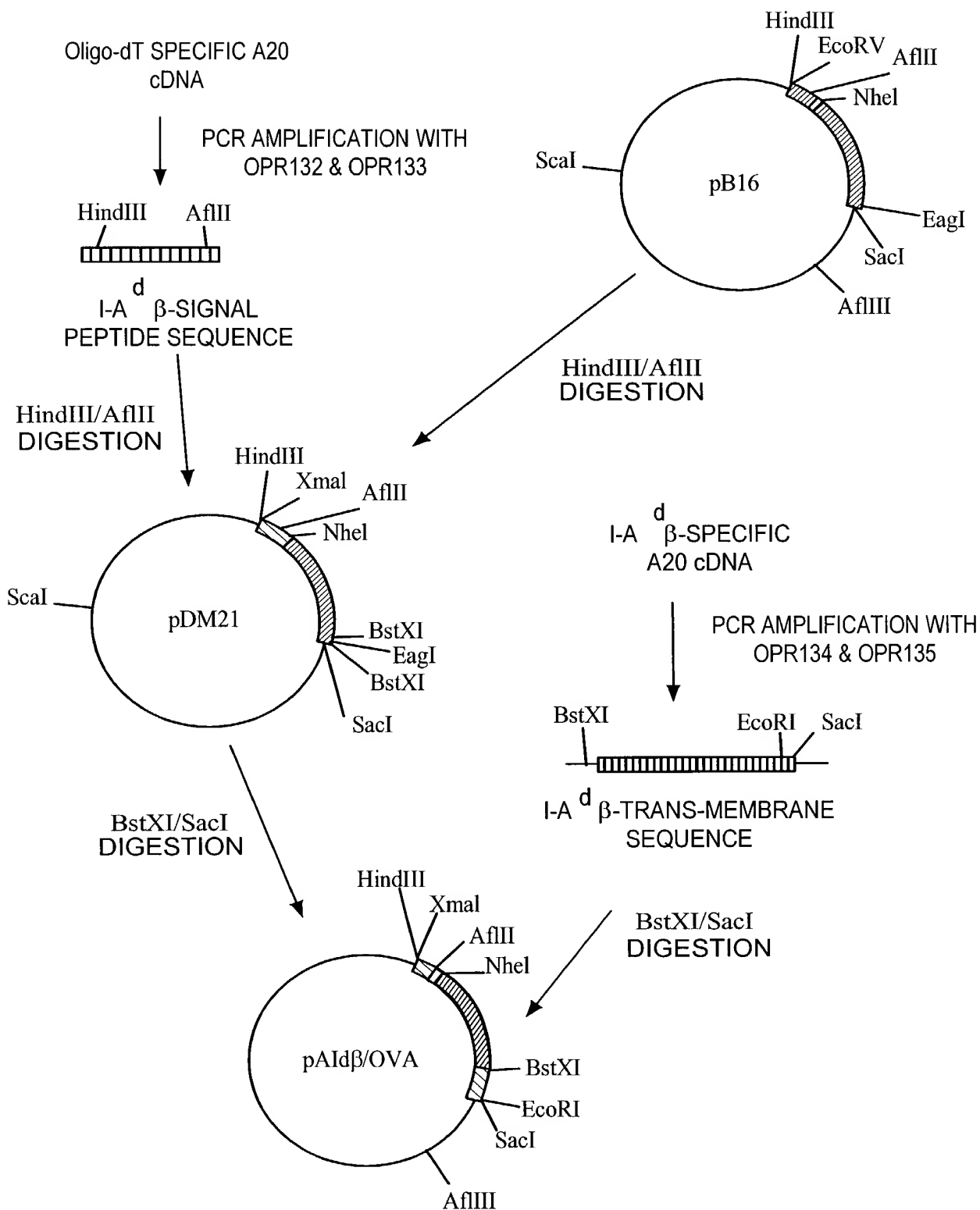


FIG. 17B

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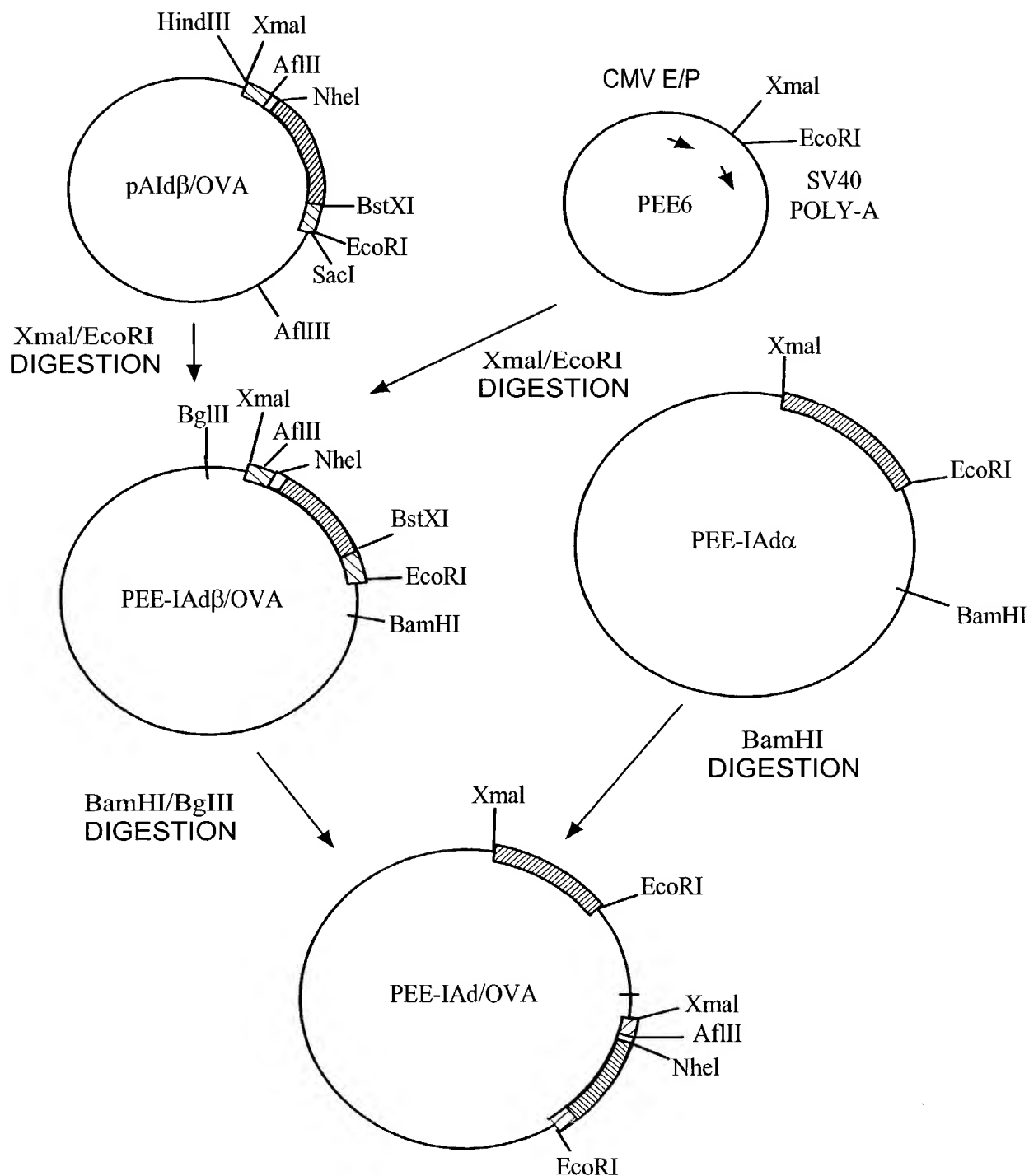


FIG. 17C

Title: MHC Complexes And Uses Thereof
 Inventor(s): Hing C. Wong, et al.
 USSN 09/900,379

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FULL LENGTH I-A^d α CHAIN INSERT

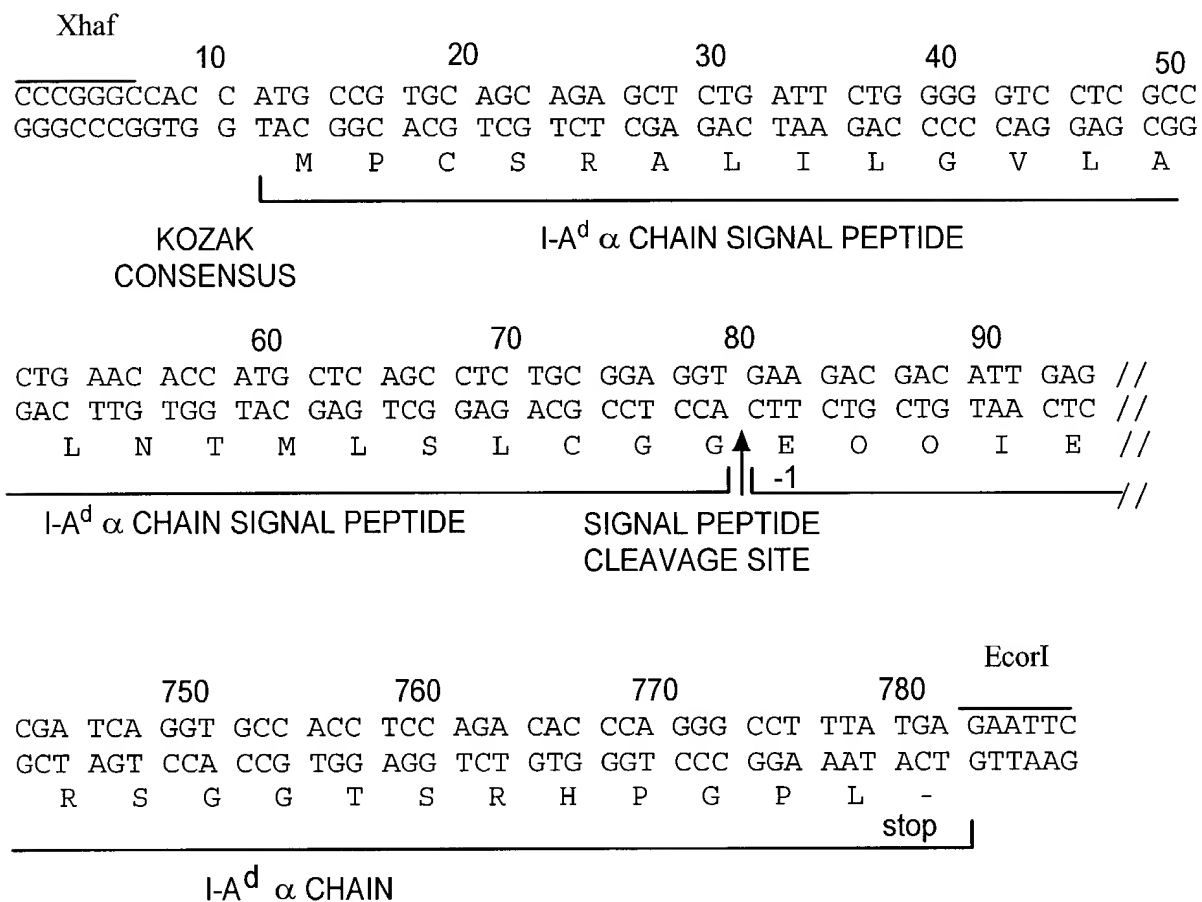


FIG. 18A

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

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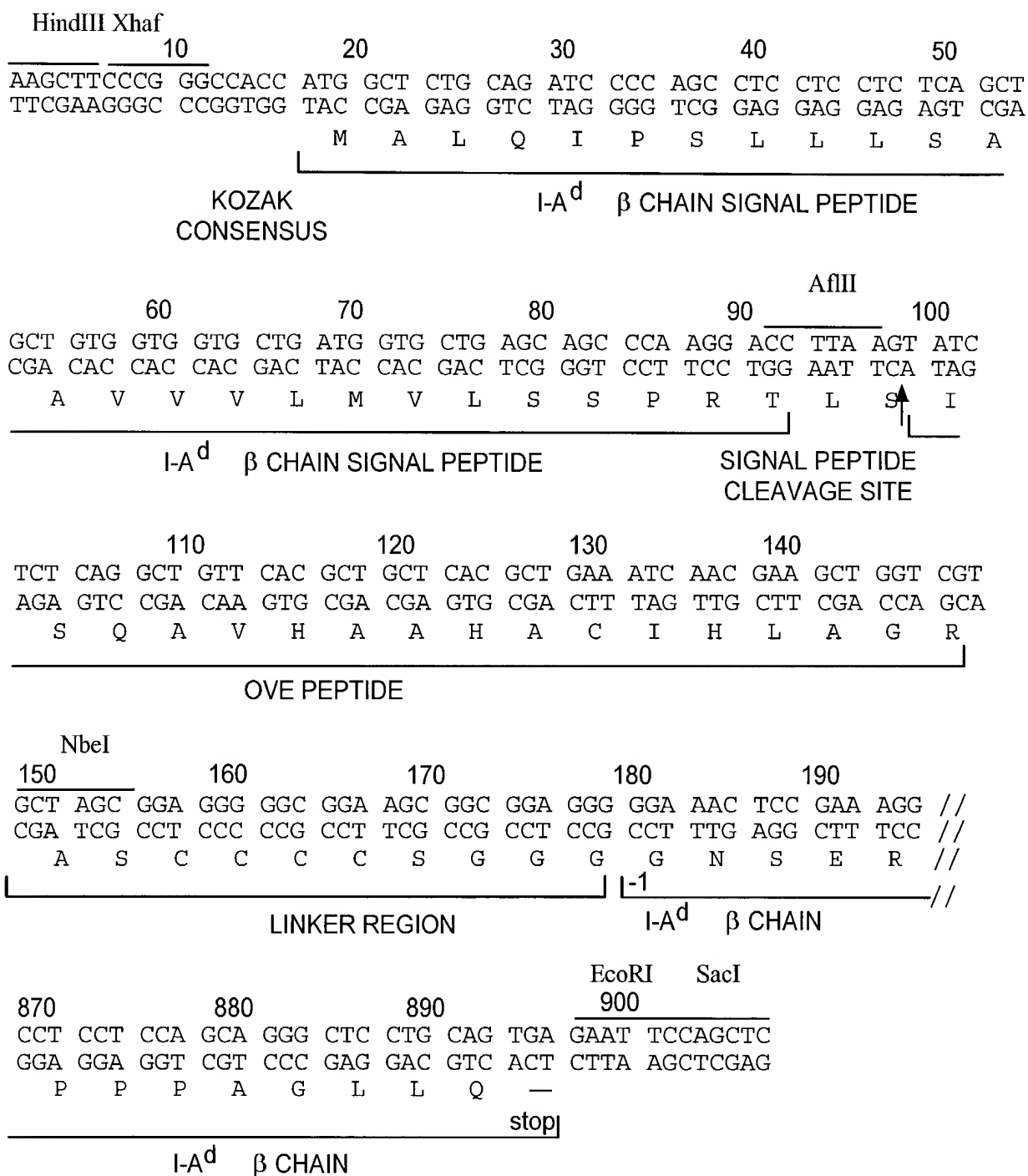
FULL LENGTH I-A^d β CHAIN INSERT

FIG. 18B

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

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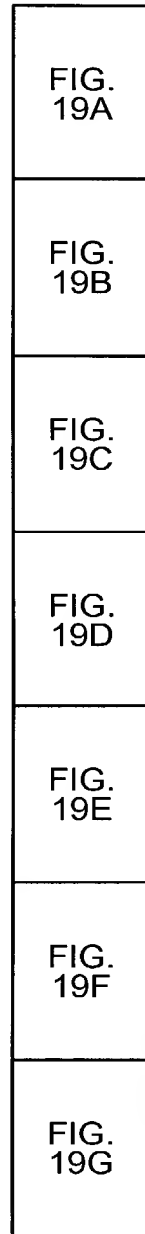


FIG. 19

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FULL-LENGTH PEPTIDE LINKED MHC EXPRESSION VECTORS

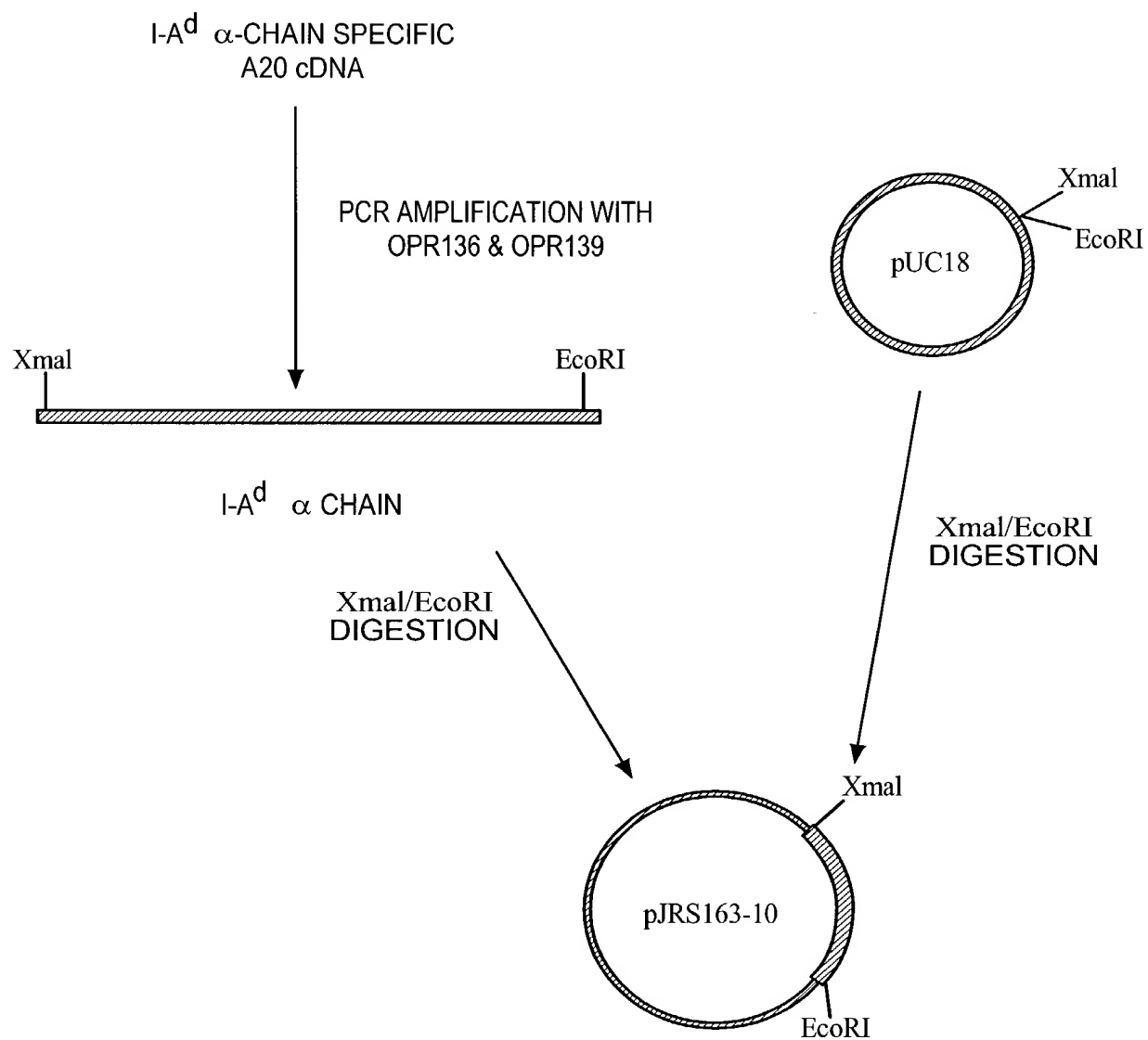


FIG. 19A

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

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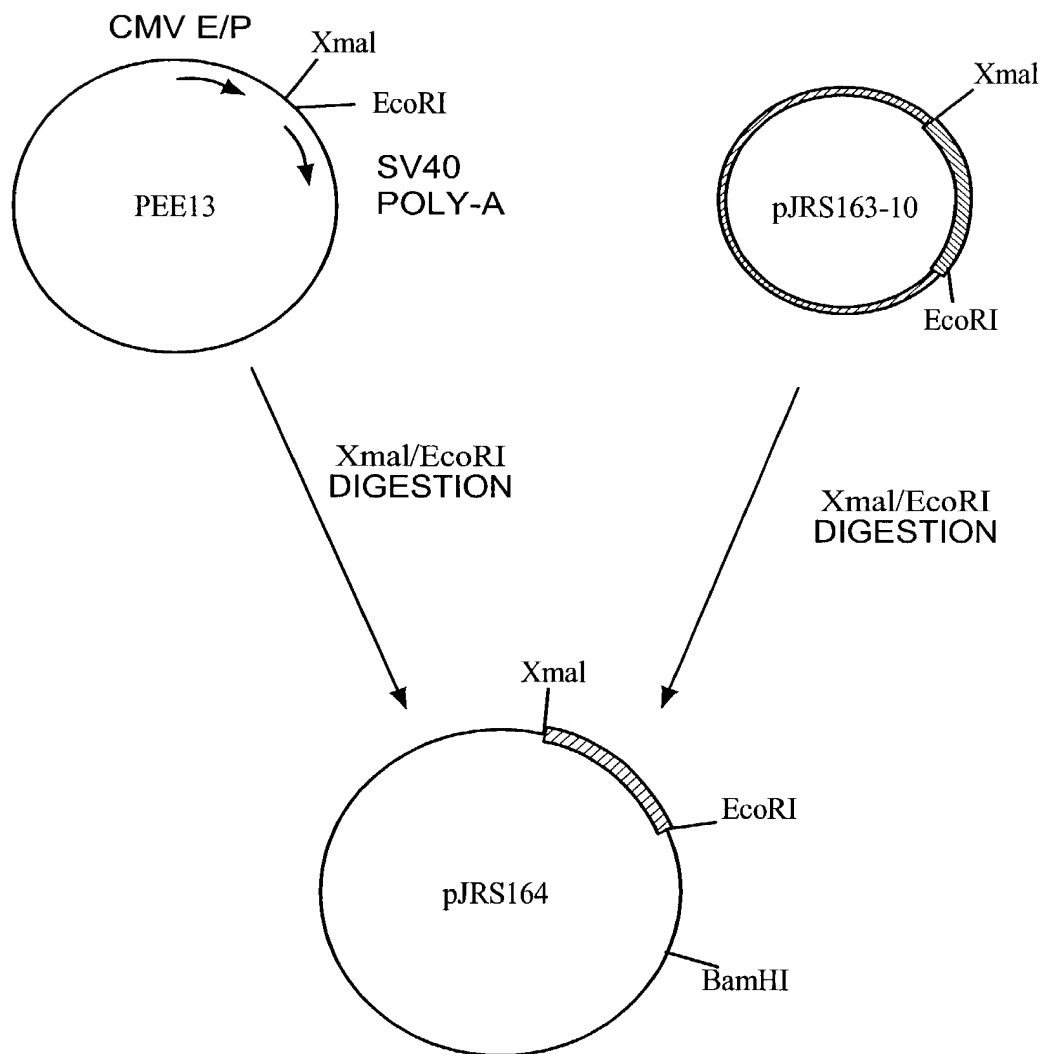


FIG. 19B

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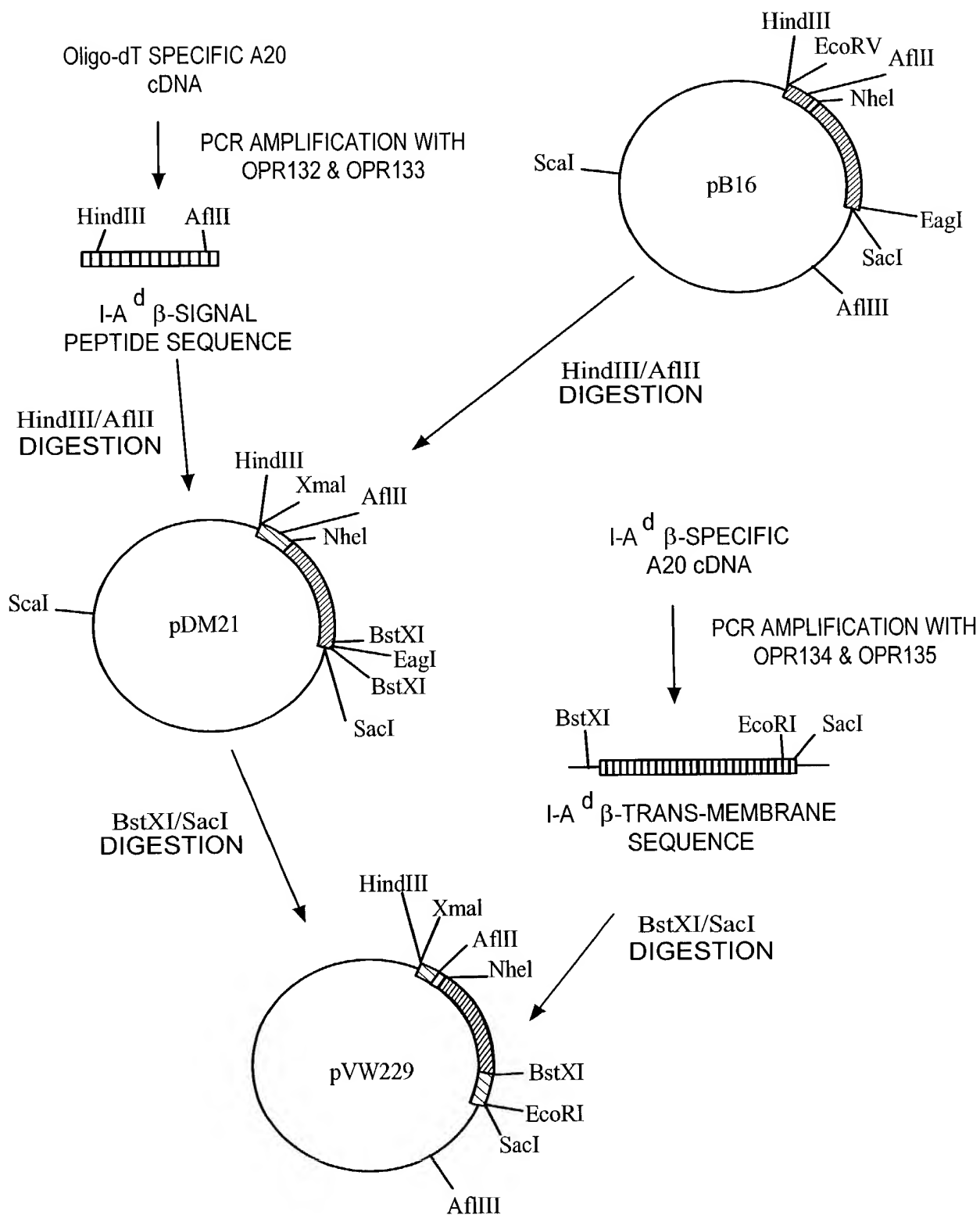


FIG. 19C

Title: MHC Complexes And Uses Thereof
Inventor(s): Hing C. Wong, et al.
USSN 09/900,379

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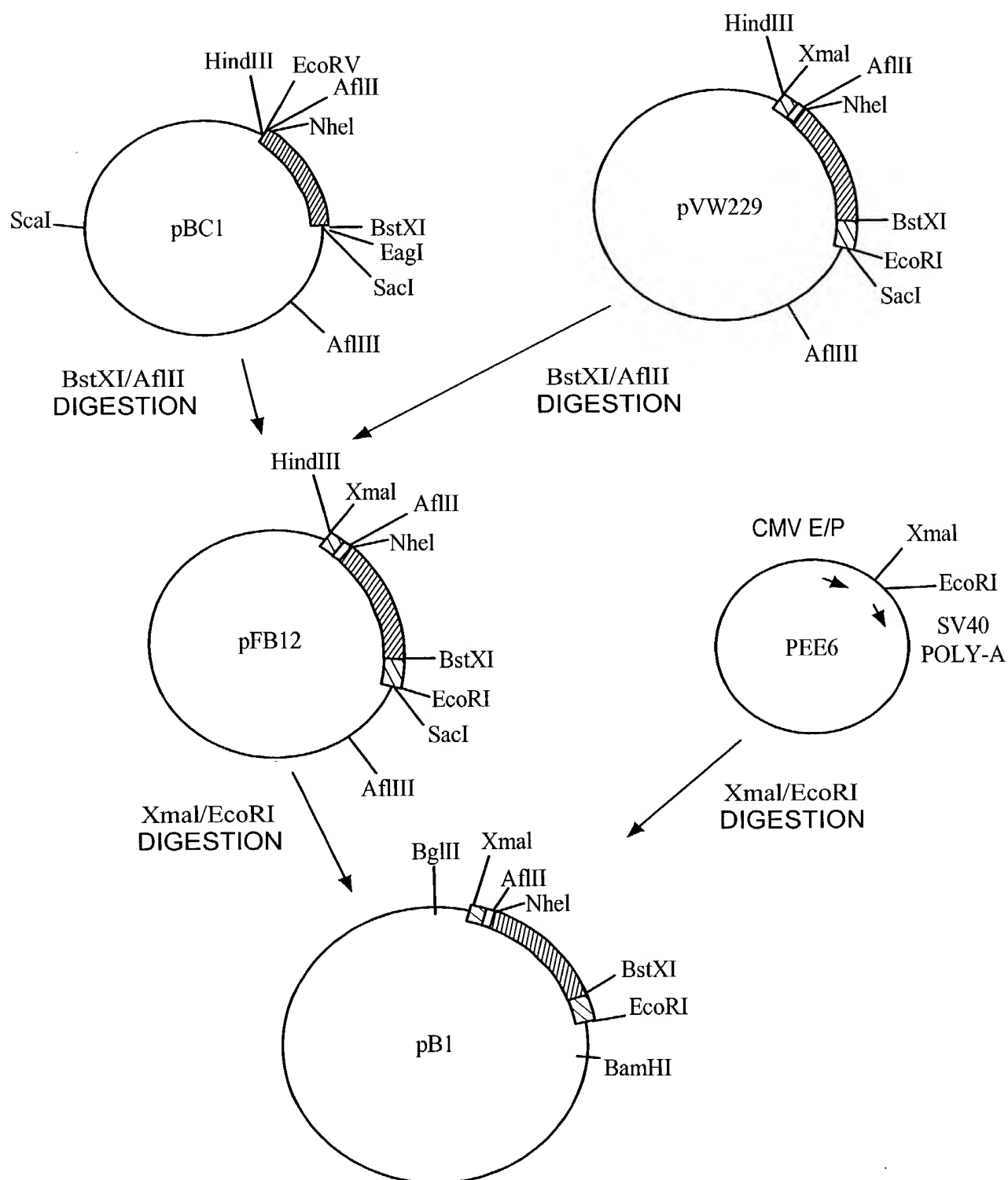


FIG. 19D

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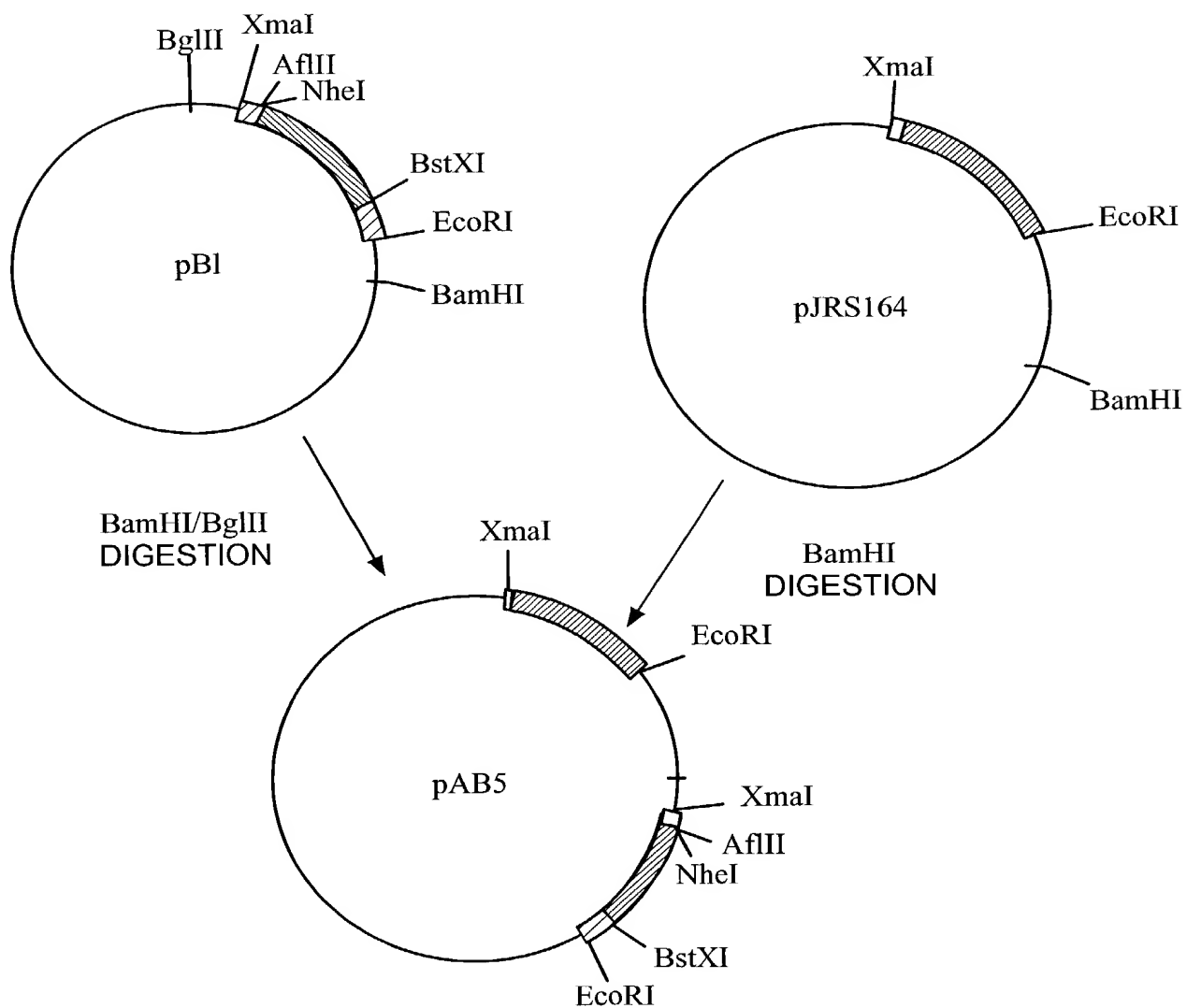


FIG. 19E

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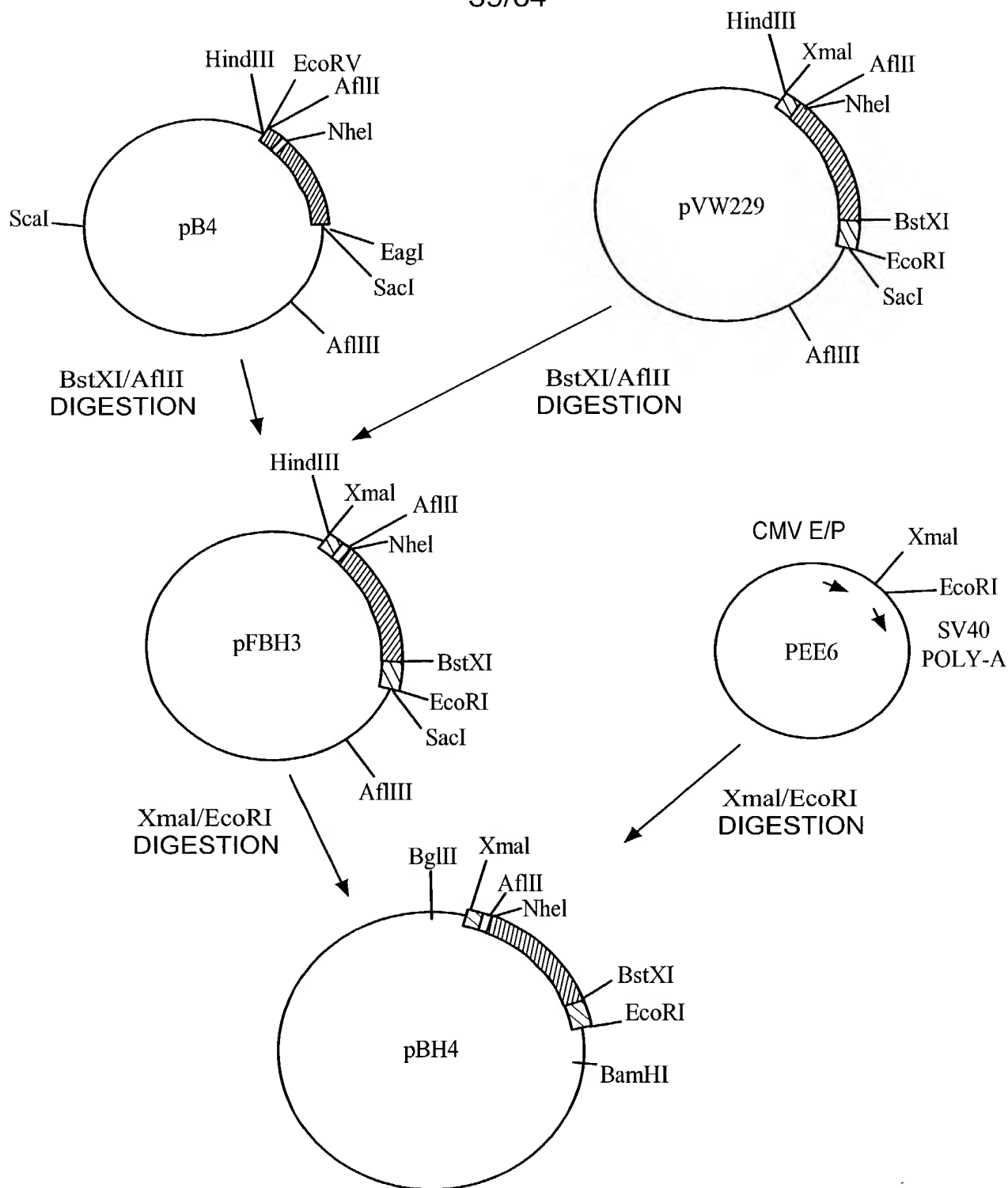


FIG. 19F

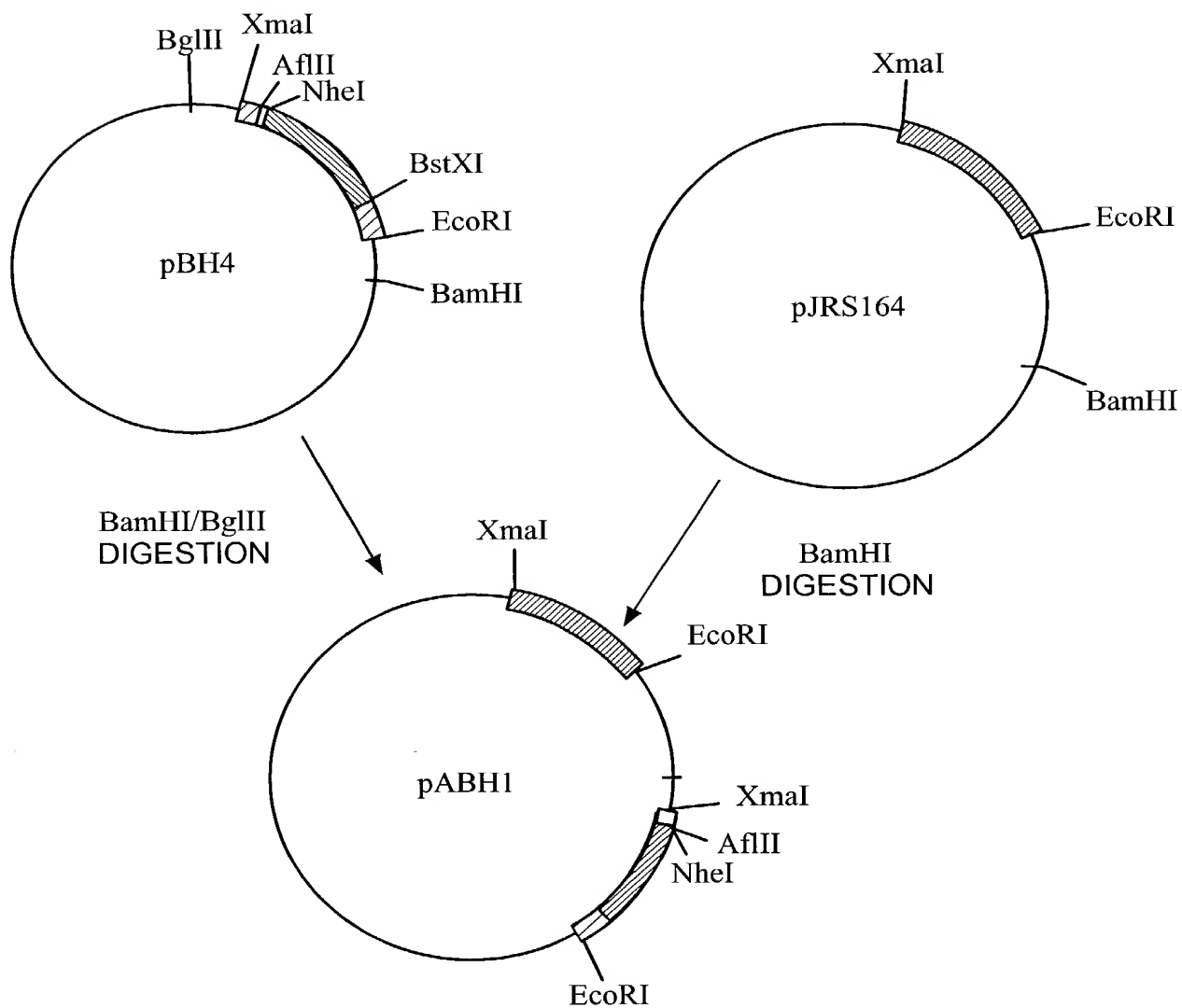


FIG. 19G

OLIGONUCLEOTIDES USED IN CLONING

OPR132

I-A^d β SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR-
HindIII/XmaI SITES

5' -CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

I-A^d β SIGNAL PEPTIDE BACK PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- AflII SITE

5' -CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

I-A^d β TRANSMEMBRANE FRONT PRIMER FOR CellTech VECTOR- BstXI SITES

5' -CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

I-A^d β TRANSMEMBRANE BACK PRIMER FOR CellTech VECTOR- SstI, EcoRI SITES

5' -CCC CCC GAG CTC GAA TCC TCA CTG CAG GAG CCC TGC TGG-3'

OPR136

I-A^d α SIGNAL PEPTIDE FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR-
HindIII/XmaI SITES

5' -CCC CCC AAG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

I-A^d α TRANSMEMBRANE PRIMER FOR CellTech VECTOR- SstI/EcoRI SITES

5' -CCC CCC GAG CTC GAA TCC TCA TAA AGG CCC TGG GTG TCT G-3'

B7-1-2F

MURINE B7-1 FRONT PRIMER WITH KOZAK CONSENSUS FOR CellTech VECTOR- NotI SITES

5' -CCC CCC CCG CGG CCG CCC CAC CAT GGG ACT GAG TAA CAT TCT
C-3'

B7-1-2B

MURINE B7-1 BACK PRIMER FOR CellTech VECTOR- NotI SITE

5' -CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

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NSO/ClassII/OVA CLONES STIMULATE IL-2
PRODUCTION FROM DO11.10

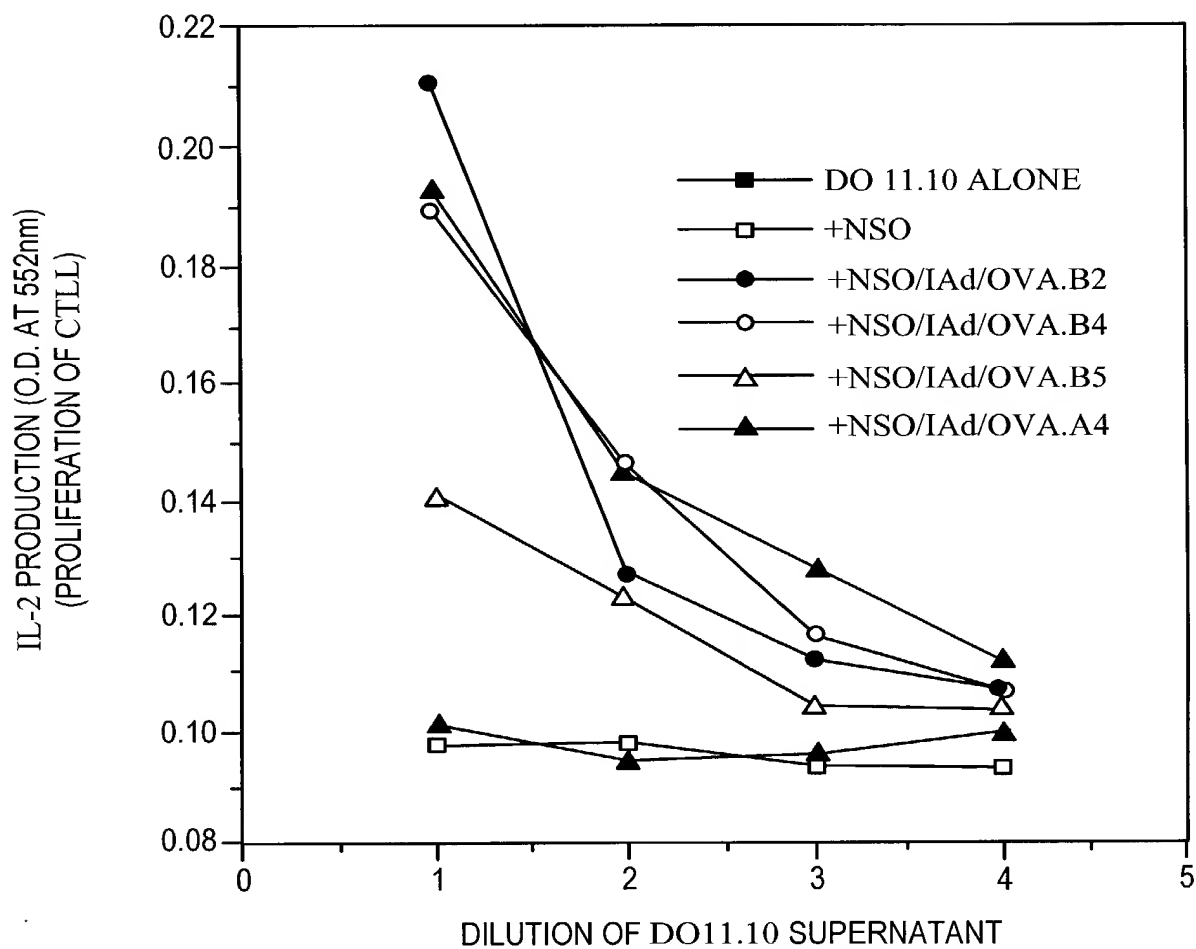


FIG. 21

Title: MHC Complexes And Uses Thereof

Inventor(s): Hing C. Wong, et al.

USSN 09/900,379

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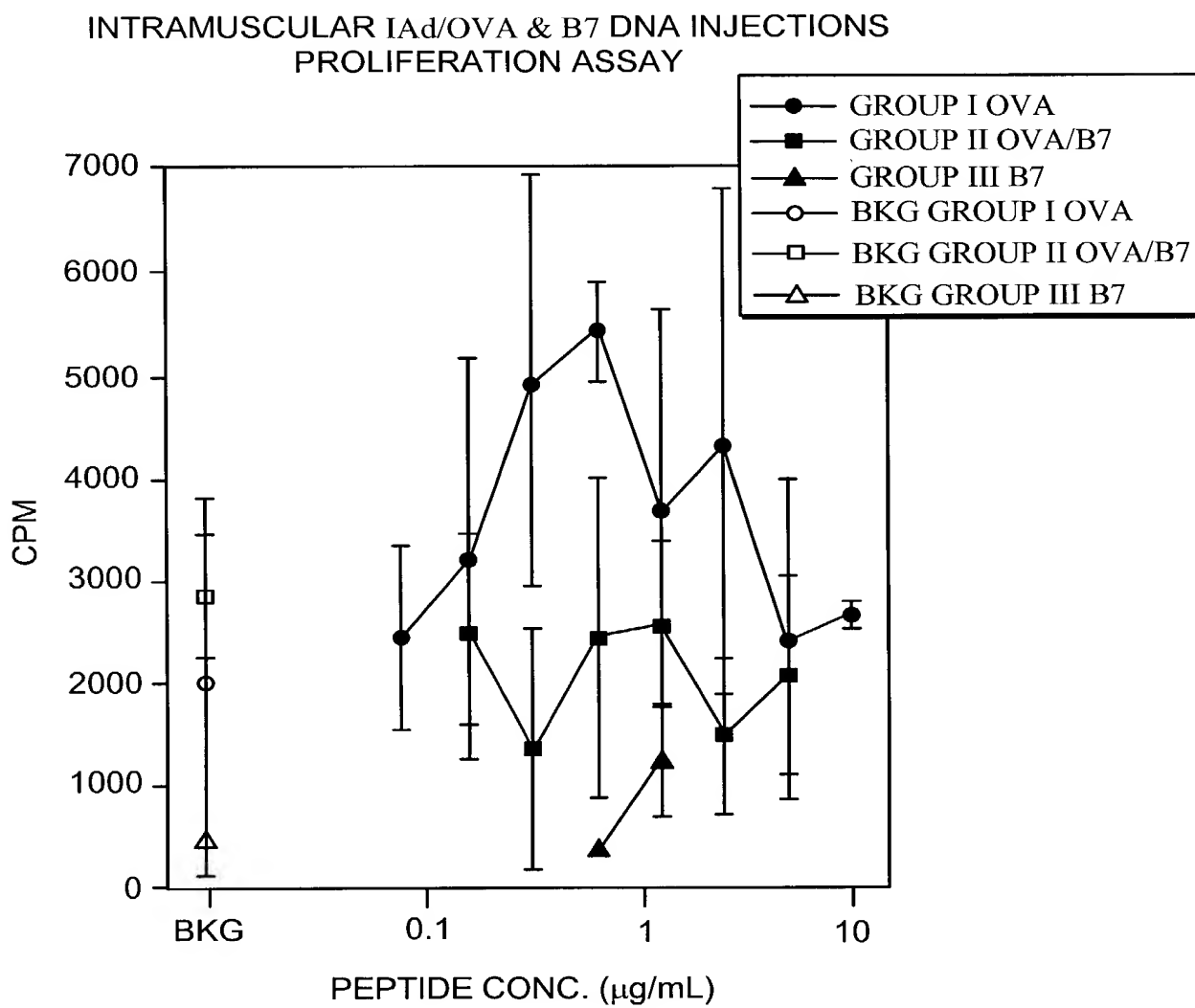


FIG. 22

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INTRADERMAL IAd/OVA & IAd/HEL DNA INJECTIONS
PROLIFERATION ASSAY
4,7 & 14 DAYS POST INJECTION

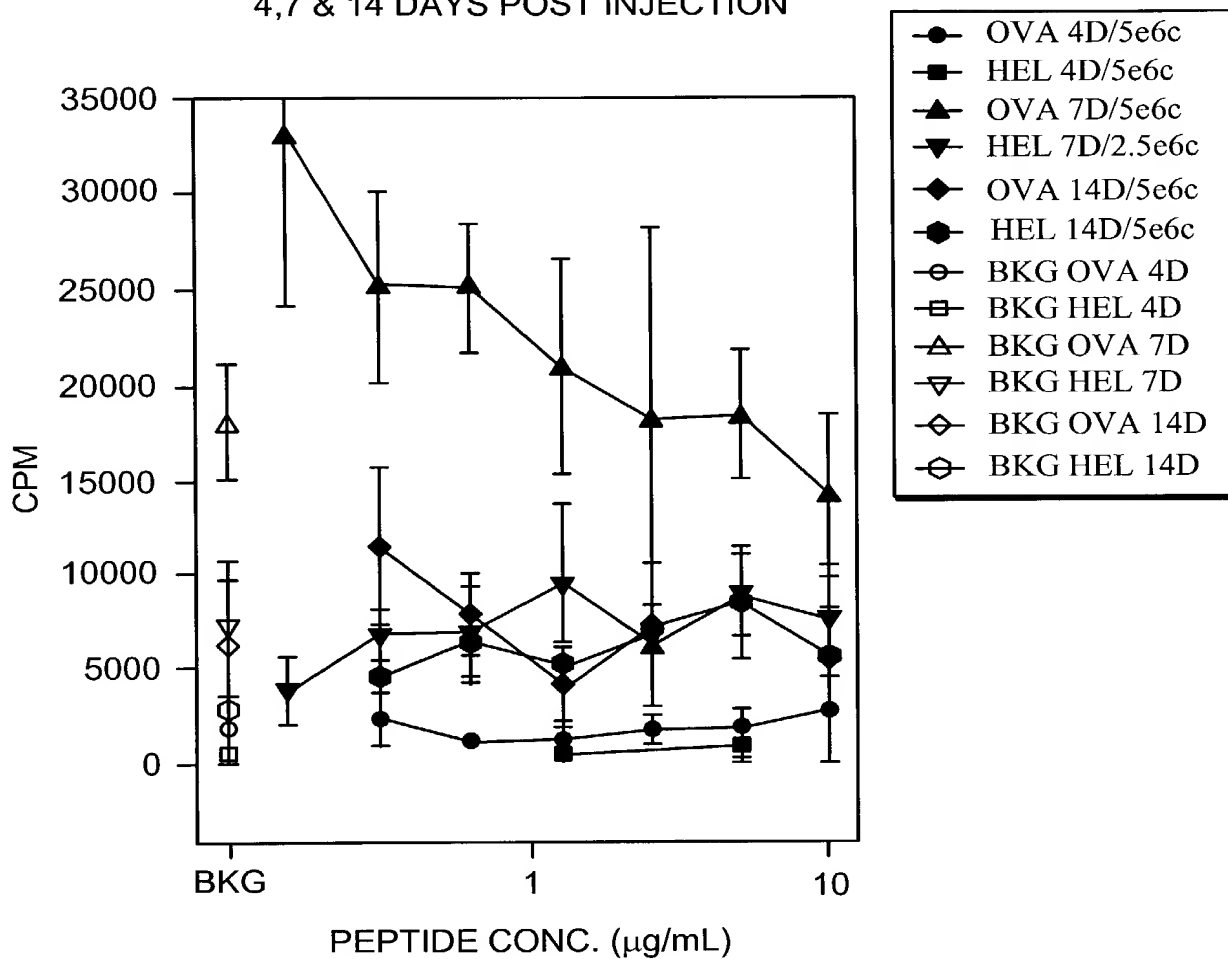
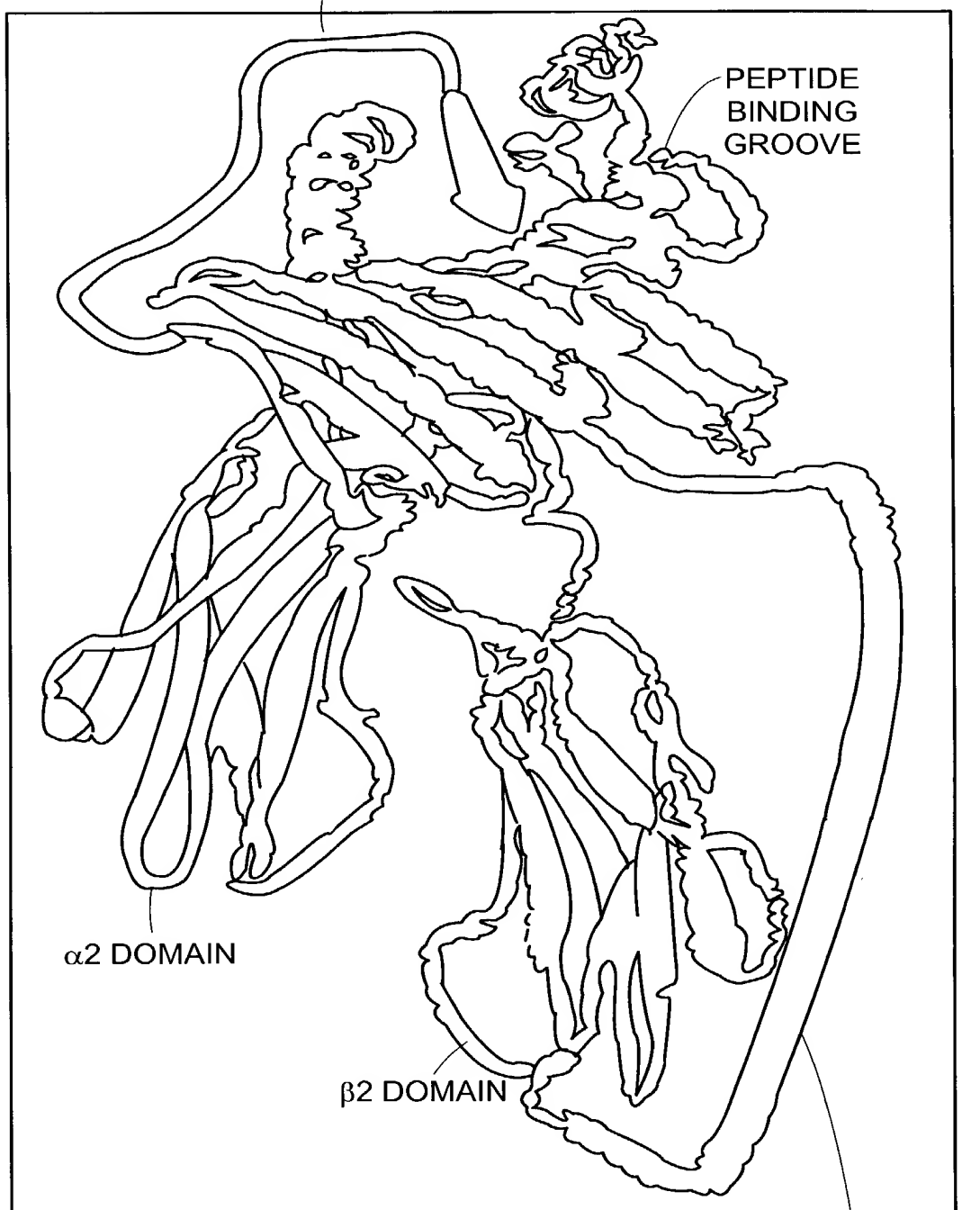


FIG. 23

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LINKER SEQUENCE LINKED
 TO PRESENTING PEPTIDE



SINGLE CHAIN
 LINKER SEQUENCE

FIG. 24

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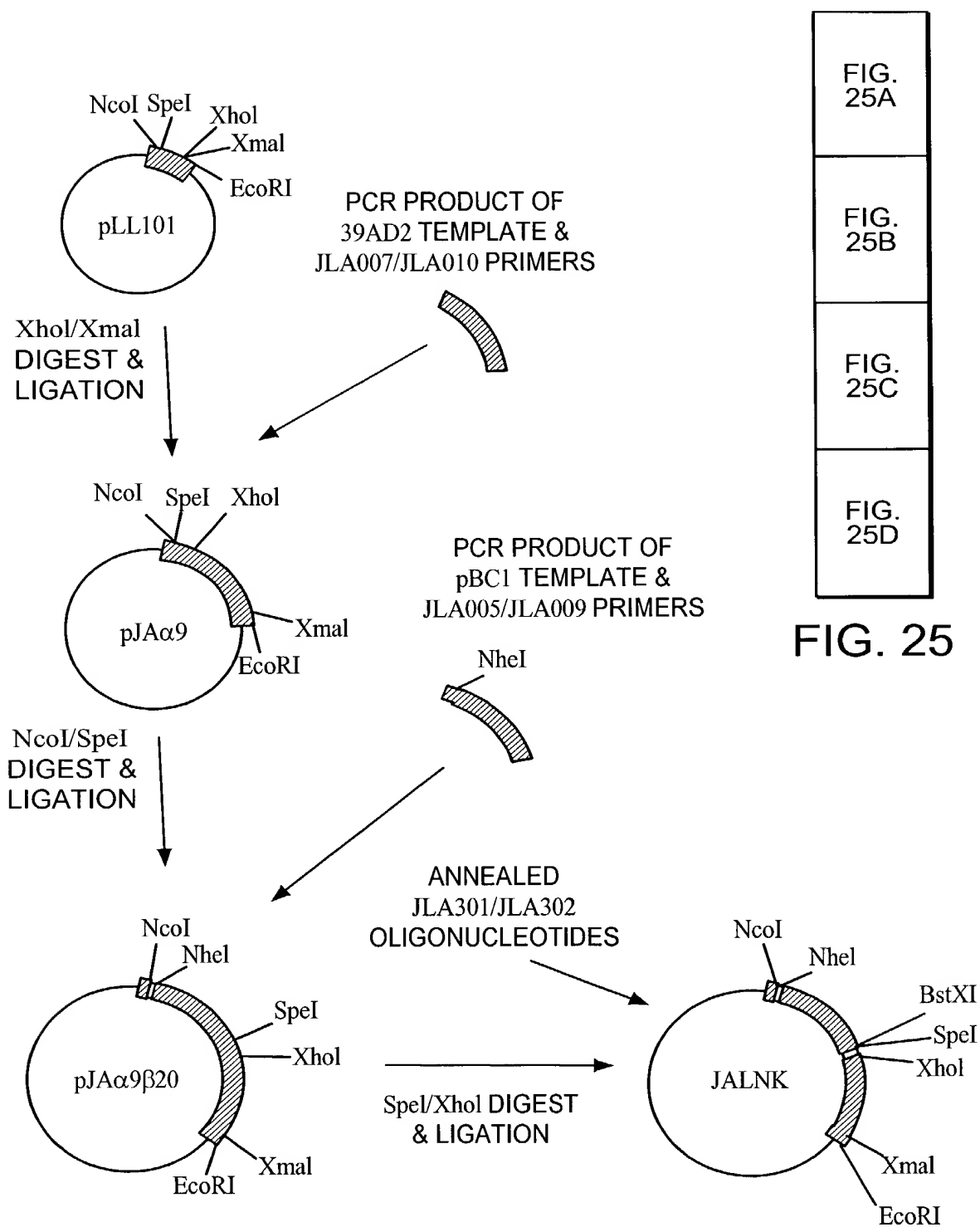
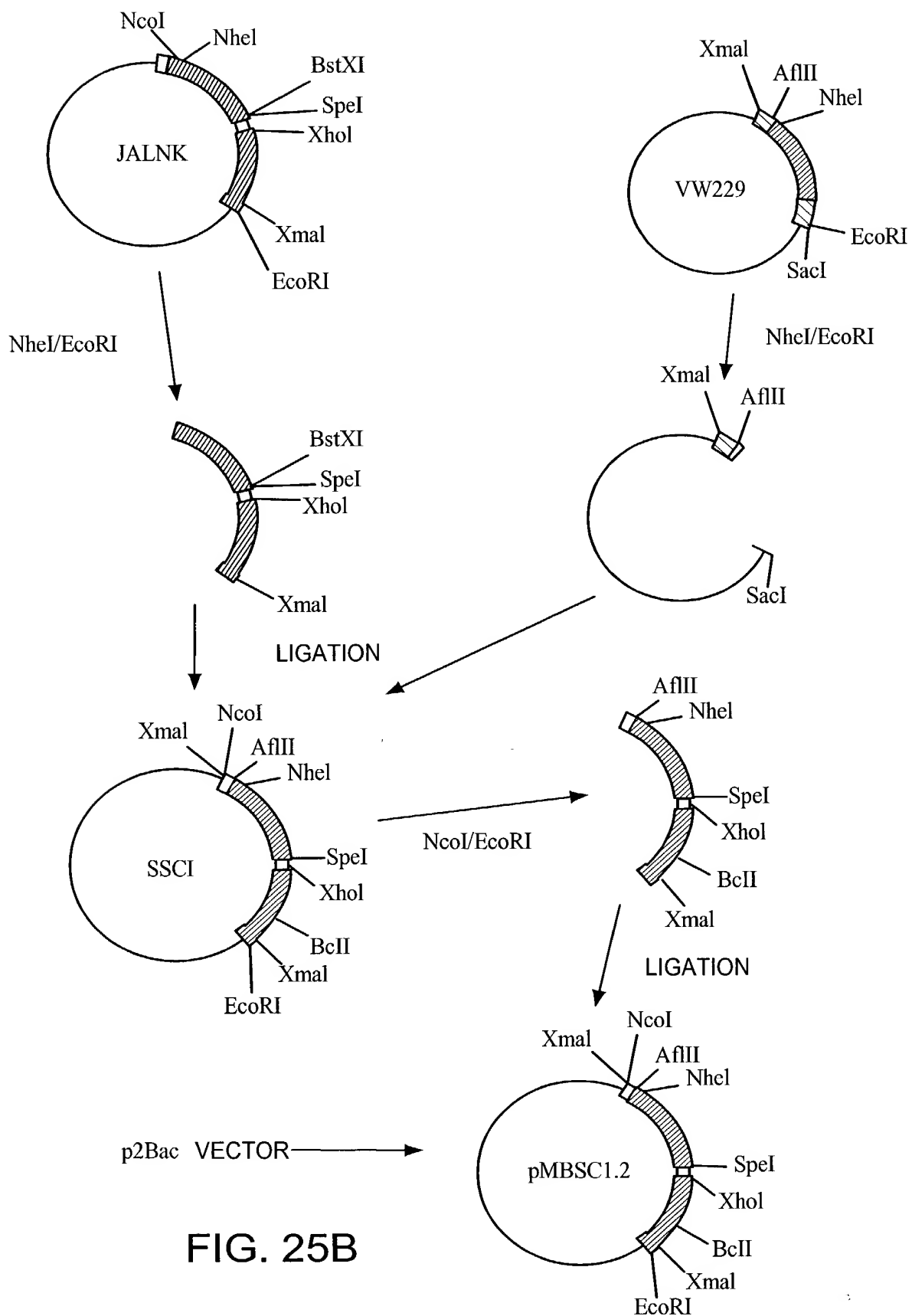


FIG. 25

FIG. 25A

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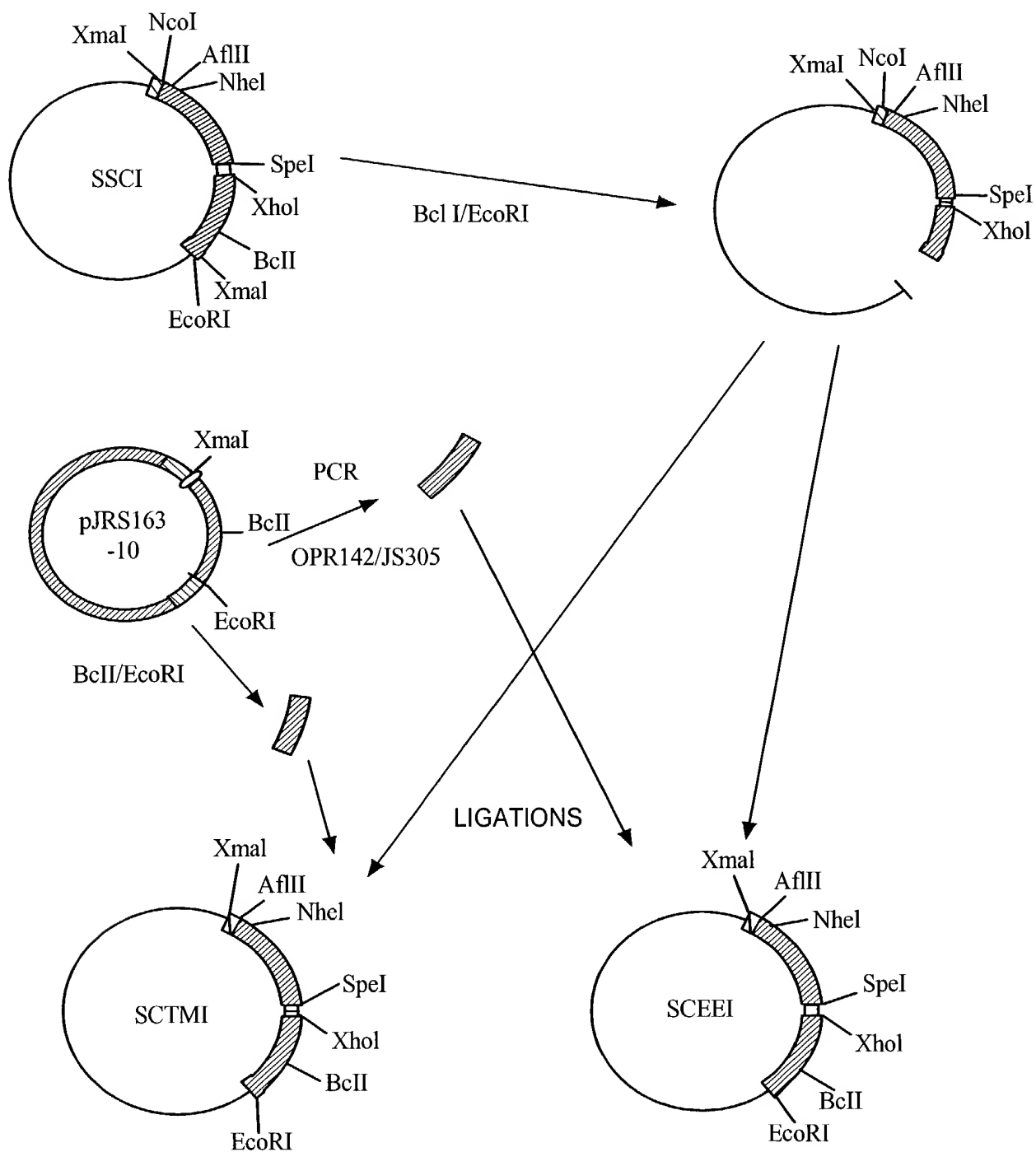


FIG. 25C

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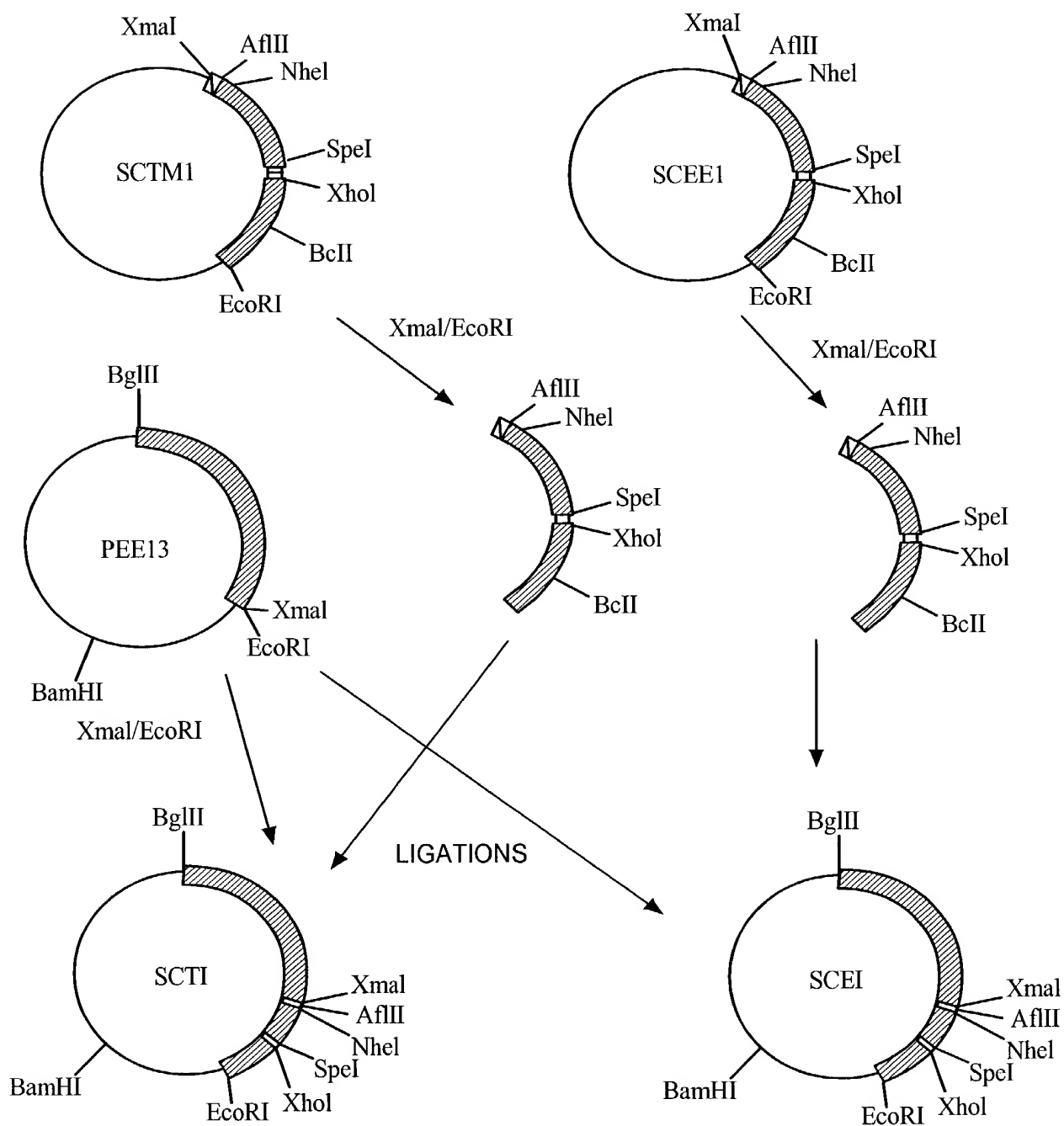


FIG. 25D

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JLA-005

5' -CCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5' -CCCGGGGCCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5' -CCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010

5' -CCCCCCCCCGGGACCAAGTGTTTCAGAACCGGCTCCTC-3'

JLA-301

5' -TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-
ACCACCACCGCCGCTGCCACCGCCACCA-3'

JLA-302

5' -CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-
TGGCGGCGGTTCTGGCGGTGGCGGTTCC-3'

OPR-142

5' -CTTGGGAATCTTGACTAAGAGG-3'

JS-305

5' -CAGGTCGAATTCTCATTCCATCGGCATGTACTCTTCTT-
CCTCCCAGTGTTTCAGAACCGG-3'

FIG. 26

FIG.
27AFIG.
27BFIG.
27CFIG.
27D

FIG. 27

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FIG. 27A

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```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG AGT CGA CGA CAC CAC
      M   A   L   Q   I   P   S   L   L   L   S   A   A   V   V>
<----- I-Ad β CHAIN LEADER ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V   L   M   V   L   S   S   P   R   T   L   S   I   S   Q   A>
-----><-----

100      110      120      130      140
  *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V   H   A   A   H   A   E   I   N   E   A   G   R   A   S   G>
----- OVA 323-339 -----><-----

      150      160      170      180      190
      *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G   G   G   S   G   G   G   G   N   S   E   R   H   F   V   V>
-- 10 AMINO ACID LINKER --><----- I-Ad β-1 DOMAIN ----->

      200      210      220      230      240
      *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
      Q   F   K   G   E   C   Y   Y   T   N   G   T   Q   R   I   R>
-----><-----

      250      260      270      280      290
      *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
      L   V   T   R   Y   I   Y   N   R   E   E   Y   V   R   Y   D>
-----><-----

      300      310      320      330
      *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
      S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D>
-----><-----

340      350      360      370      380
  *      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCC GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
      A   E   Y   W   N   S   Q   P   E   I   L   E   R   T   R   A>
-----><-----

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FIG. 27B

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390 *	400 *	410 *	420 *	430 *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC				
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG				
E V D T A C R H N Y E G P E T S>				

440 *	450 *	460 *	470 *	480 *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC				
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG				
T S L R R L E Q P N V A I S L S>				
----- I-Ad β-1 DOMAIN -----><----- I-Ad β-2 DOMAIN -----				
490 *	500 *	510 *	520 *	530 *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA				
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT				
R T E A L N H H N T L V C S V T>				

540 *	550 *	560 *	570 *	
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG				
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC				
D F Y P A K I K V R W F R N G Q>				

580 *	590 *	600 *	610 *	620 *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC				
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG				
E E T V G V S S T Q L I R N G D>				

630 *	640 *	650 *	660 *	670 *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA				
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT				
W T F Q V L V M L E N T P H Q G>				

680 *	690 *	700 *	710 *	720 *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC				
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG				
E V V T C H V E H P S L A S P I>				
----- I-Ad β-2 DOMAIN -----				
730 *	740 *	750 *	760 *	770 *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC				
TCA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG				
T V E W T S G G G G S G G G S G G G S>				
----- 24 AMINO ACID LINKER -----				

FIG. 27C

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```

      780      790      800      810
      *      *      *      *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC ACT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
G  G  G  G  S  G  G  G  G  S  S  S  E  D  D  I>
-----><-----

820      830      840      850      860
*      *      *      *      *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CGG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
E  A  D  H  V  G  F  Y  G  T  T  V  Y  Q  S  P>
----- I-Ad  $\alpha$ -1 DOMAIN -----

      870      880      890      900      910
      *      *      *      *      *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTC TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G  D  I  G  Q  Y  T  H  E  F  D  G  D  E  L  F>
-----

      920      930      940      950      960
      *      *      *      *      *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y  V  D  L  D  K  K  K  T  V  W  R  L  P  E  F>
-----

      970      980      990      1000      1010
      *      *      *      *      *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G  Q  L  I  L  F  E  P  Q  G  G  L  Q  N  I  A>
-----

      1020      1030      1040      1050
      *      *      *      *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A  E  K  H  N  L  G  I  L  T  K  R  S  N  F  T>
----- I-Ad  $\alpha$ -1 DOMAIN -----

1060      1070      1080      1090      1100
*      *      *      *      *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P  A  T  N  E  A  P  Q  A  T  V  F  P  K  S  P>
-----><----- I-Ad  $\alpha$ -2 DOMAIN -----

      1110      1120      1130      1140      1150
      *      *      *      *      *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V  L  L  G  Q  P  N  T  L  I  C  F  V  D  N  T>
-----
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1160 *	1170 *	1180 *	1190 *	1200 *
TTC CCA GCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC				
AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG				
F P P V I N I T W L R N S K S V>				

1210 *	1220 *	1230 *	1240 *	1250 *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC				
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG				
T D G V Y E T S F L V N R D H S>				

1260 *	1270 *	1280 *	1290 *	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT				
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA				
F H K L S Y L T F I P S D D D I>				

1300 *	1310 *	1320 *	1330 *	1340 *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA				
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT				
Y D C K V E H W G L E E P V L K>				
----- I-Ad α -2 DOMAIN -----				
1350 *	1360 *	1370 *	1380 *	
CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG				
GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTA GTG ATC				
H W S R A S H H H H H H *>				
-----><----- 6 X HIS TAG----->				

FIG. 27D

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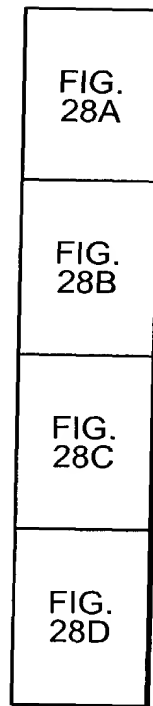


FIG. 28

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FIG. 28A

```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TGA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M  A  L  Q  I  P  S  L  L  L  S  A  A  V  V>
<----- I-Ad β CHAIN LEADER ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V  L  M  V  L  S  S  P  R  T  L  S  I  S  Q  A>
-----><-----

    100      110      120      130      140
    *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V  H  A  A  H  A  E  I  N  E  A  G  R  A  S  G>
----- OVA 323-339 -----><-----

    150      160      170      180      190
    *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G  G  G  S  G  G  G  G  N  S  E  R  H  F  V  V>
---10 AMINO ACID LINKER--><----- I-Ad β-1 DOMAIN ----->

    200      210      220      230      240
    *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
      Q  F  L  G  E  C  Y  Y  T  N  G  T  Q  R  I  R>
-----><-----

    250      260      270      280      290
    *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
      L  V  T  R  Y  I  Y  N  R  E  E  Y  V  R  Y  D>
-----><-----

    300      310      320      330
    *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
      S  D  V  G  E  Y  R  A  V  T  E  L  G  R  P  D>
-----><-----

    340      350      360      370      380
    *      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
      A  E  Y  W  N  S  Q  P  E  I  L  E  R  T  R  A>
-----><-----

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FIG. 28B

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390 *	400 *	410 *	420 *	430 *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC				
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG				
E V D T A C R H N Y E G P E T S>				

440 *	450 *	460 *	470 *	480 *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC				
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG				
T S L R R L E Q P N V A I S L S>				
---- I-Ad β-1 DOMAIN		-----X----- I-Ad β-2 DOMAIN		

490 *	500 *	510 *	520 *	530 *
AGG ACA GAG GCC CTC AAG CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA				
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT				
R T E A L N H H N T L V C S V T>				

540 *	550 *	560 *	570 *	
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG				
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC				
D F Y P A K I K V R W F R N G Q>				

580 *	590 *	600 *	610 *	620 *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC				
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG				
E E T V G V S S T Q L I R N G D>				

630 *	640 *	650 *	660 *	670 *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA				
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT				
W T F Q V L V M L E M T P H Q G>				

680 *	690 *	700 *	710 *	720 *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC				
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG				
E V Y T C H V E H P S L K S P I>				
----- I-Ad β-2 DOMAIN -----				

730 *	740 *	750 *	760 *	770 *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC				
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG				
T V E W T S G G G G S G G G G S>				
----- 24 AMINO ACID LINKER -----				

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FIG. 28C

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780 *					790 *					800 *					810 *									
GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	ATT									
CCA	CCG	CCG	CCA	AGA	CCG	CCA	CCG	CCA	AGG	AGC	TCA	CTT	CTG	CTG	TAA									
G	G	G	G	S	G	G	G	G	S	S	S	E	D	D	I>									
-----><-----																								
820 *					830 *					840 *					850 *					860 *				
GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	CCT									
CTC	CGG	CTG	GTG	CAT	CCG	AAG	ATA	CCA	TGT	TGA	CAA	ATA	GTC	AGA	GGA									
E	A	D	H	V	G	F	Y	G	T	T	V	Y	Q	S	P>									
----- I-Ad α-1 DOMAIN -----																								
870 *					880 *					890 *					900 *					910 *				
GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TTG	TTC									
CCT	CTG	TAA	CCG	GTC	ATG	TGT	GTA	CTT	AAA	CTA	CCA	CTA	CTC	AAC	AAG									
G	D	I	G	Q	Y	T	H	E	F	D	G	D	E	L	F>									

920 *					930 *					940 *					950 *					960 *				
TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	GTC	TGG	AGG	CTT	CCT	GAG	TTT									
ATA	CAC	CTG	AAC	CTA	TTC	TTC	TTT	TGA	CAG	ACC	TCC	GAA	GGA	CTC	AAA									
Y	V	D	L	D	K	K	K	T	V	W	R	L	P	E	F>									

970 *					980 *					990 *					1000 *					1010 *				
GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	GGT	GGA	CTG	CAA	AAC	ATA	GCT									
CCG	GTT	AAC	TAT	GAG	AAA	CTC	GGG	GTT	CCA	CCT	GAC	GTT	TTG	TAT	CGA									
G	Q	L	I	L	F	E	P	Q	G	G	L	Q	N	I	A>									

1020 *					1030 *					1040 *					1050 *									
GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TTC	ACC									
CGT	CTT	TTT	GTG	TTG	AAC	CCT	TAG	AAC	TGA	TTC	TCC	AGT	TTA	AAG	TGG									
A	E	K	H	N	L	G	I	L	T	K	R	S	N	F	T>									
----- I-Ad α-1 DOMAIN -----																								
1060 *					1070 *					1080 *					1090 *					1100 *				
CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	CCT									
GGT	CGA	TGG	TTA	CTC	CGA	GGA	GTT	CGC	TGA	CAC	AAG	GGG	TTC	AGG	GGA									
P	A	T	N	E	A	P	Q	A	T	V	F	P	K	S	P>									
-----><----- I-Ad α-2 DOMAIN -----																								
1110 *					1120 *					1130 *					1140 *					1150 *				
GTG	CTG	CTG	GGT	CAG	CCC	AAC	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	ATC									
CAC	GAC	GAC	CCA	GTC	GGG	TTG	TGG	GAA	TAG	ACG	AAA	CAC	CTG	TTG	TAG									
V	L	L	G	Q	P	N	T	L	I	C	F	V	D	N	I>									

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1160 *	1170 *	1180 *	1190 *	1200 *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTG				
AAG GGT GGA CAC TAG TTG TAG TGT ACG GAG TCT TTA TCG TTC AGT CAG				
F P P V I N I T W L R N S K S V>				
1210 *	1220 *	1230 *	1240 *	1250 *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC				
TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG				
T D G V Y E T S F L V N R D H S>				
1260 *	1270 *	1280 *	1290 *	
TTC CAC AAG CTG TCT TAT CTC ACG TTC ATC CCT TCT GAT GAT GAC ATT				
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA				
F H K L S Y L T F I P S D D D I>				
1300 *	1310 *	1320 *	1330 *	1340 *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA				
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGG CAA GAC TTT				
Y D C K V E H W G L E E P V L X>				
----- I-Ad α -2 DOMAIN -----				
1350 *	1360 *	1370 *	1380 *	1390 *
CAC TCG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT				
GTG ACC CTT GGA CTC TAA GGT CGG GGG TAC AGT CTC GAC TGT CTT TGA				
H N E P E I P A P M S E L T E T>				
-----><----- I-Ad α -TM DOMAIN -----				
1400 *	1410 *	1420 *	1430 *	1440 *
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG				
CAC CAC ACA CGG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC				
V V C A L G L S V G L V G I V V>				
1450 *	1460 *	1470 *	1480 *	1490 *
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA				
CCG TGG TAG AAG TAG TAA GTT CCG GAG GCT AGT CCA CCG TGG AGG TCT				
G T I F I I Q G L R S G G T S R>				
1500 *				
CAC CCA GGC CCT TTA TGA				
GTG GGT CCC GGA AAT ACT				
H P G P L *>				
-- I-Ad α -TM DOMAIN ->				

FIG. 28D

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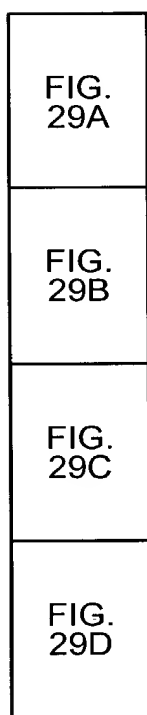


FIG. 29

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FIG. 29A

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      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M  A  L  Q  I  P  S  L  L  L  S  A  A  V  V>
<----- I-Ad β CHAIN LEADER ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
V  L  M  V  L  S  S  P  R  T  L  S  I  S  Q  A>
-----><-----

100      110      120      130      140
*      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CGA GCA CGA TCG CCT
V  H  A  A  H  A  E  I  N  E  A  G  R  A  S  G>
----- OVA 323-339 -----><-----

150      160      170      180      190
*      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
G  G  G  S  G  G  G  G  N  S  E  R  H  F  V  V>
---10 AMINO ACID LINKER--><----- I-Ad β-1 DOMAIN ----->

200      210      220      230      240
*      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
Q  F  K  G  E  C  Y  Y  T  N  G  T  Q  R  I  R>
-----><-----

250      260      270      280      290
*      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
L  V  T  R  Y  I  Y  N  R  E  E  Y  V  R  Y  D>
-----><-----

300      310      320      330
*      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG GCG CAC TGG CTC GAC CCC GCC GGT CTG
S  D  V  G  E  Y  R  A  V  T  E  L  G  R  P  D>
-----><-----

340      350      360      370      380
*      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
A  E  Y  W  N  S  Q  P  E  I  L  E  R  T  R  A>
-----><-----

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FIG. 29B

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390 *	400 *	410 *	420 *	430 *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC				
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG				
E V D T A C R H N Y E G P E T S>				

440 *	450 *	460 *	470 *	480 *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC				
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG				
T S L R R L E Q P N V A I S L S>				
---- I-Ad β -1 DOMAIN		-----><----- I-Ad β -2 DOMAIN		

490 *	500 *	510 *	520 *	530 *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA				
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT				
R T E A L N H H N T L V C S V T>				

540 *	550 *	560 *	570 *	
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG				
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC				
D F Y P A K I K V R W F R N G Q>				

580 *	590 *	600 *	610 *	620 *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC				
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG				
E E T V G V S S T Q L I R N G D>				

630 *	640 *	650 *	660 *	670 *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA				
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT				
W T F Q V L V M L F M T P H Q G>				

680 *	690 *	700 *	710 *	720 *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC				
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG				
E V Y T C H V E H P S L K S P I>				
			----- I-Ad β -2 DOMAIN	

730 *	740 *	750 *	760 *	770 *
ACT GTG GAG TGG ACT AGT GGT GGG GGT GGC AGC GGC GGT GGT GGT TCC				
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG				
T V E W T S G G G G S G G G S>				
-----><-----			24 AMINO ACID LINKER-----	

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FIG. 29C

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780 *					790 *					800 *					810 *				
GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCC	AGT	GAA	GAC	GAC	ATT				
CCA	CCG	CCG	CCA	AGA	CCG	CCA	CCG	CCA	AGG	AGC	TCA	CTT	CTG	CTG	TAA				
G	G	G	G	S	G	G	G	G	S	S	S	E	D	D	I>				
-----><-----																			
820 *			830 *			840 *			850 *			860 *							
GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	CCT				
CTC	CGG	CTG	GTG	CAT	CCG	AAG	ATA	CCA	TGT	TGA	CAA	ATA	GTC	AGA	GGA				
E	A	C	H	V	G	F	Y	G	T	T	V	Y	Q	S	P>				
-----I-Ad α -1 DOMAIN-----																			
870 *			880 *			890 *			900 *			910 *							
GGA	GAC	ATT	GGC	CAG	TAC	ACA	CAT	GAA	TTT	GAT	GGT	GAT	GAG	TTG	TTC				
CCT	CTG	TAA	CCG	GTC	ATG	TGT	GTA	CTT	AAA	CTA	CCA	CTA	CTC	AAC	AAG				
G	D	I	G	Q	Y	T	H	E	F	D	G	D	E	L	F>				

920 *			930 *			940 *			950 *			960 *							
TAT	GTG	GAC	TTG	GAT	AAG	AAG	AAA	ACT	GTC	TGG	AGG	CTT	CCT	GAG	TTT				
ATA	CAC	CTG	AAC	CTA	TTC	TTC	TTT	TGA	CAG	ACC	TCC	GAA	GGA	CTC	AAA				
Y	V	D	L	D	K	K	K	T	V	W	R	L	P	E	F>				

970 *			980 *			990 *			1000 *			1010 *							
GGC	CAA	TTG	ATA	CTC	TTT	GAG	CCC	CAA	GGT	GSA	CTG	CAA	AAC	ATA	GCT				
CCG	GTT	AAC	TAT	GAG	AAA	CTC	GGG	GTT	CCA	CCT	GAC	GTT	TTG	TAT	CGA				
G	Q	L	I	L	F	E	P	Q	G	G	L	Q	N	I	A>				

1020 *			1030 *			1040 *			1050 *										
GCA	GAA	AAA	CAC	AAC	TTG	GGA	ATC	TTG	ACT	AAG	AGG	TCA	AAT	TTC	ACC				
CGT	CTT	TTT	GTG	TTG	AAC	CCT	TAG	AAC	TGA	TTC	TCC	AGT	TTA	AAG	TGG				
A	E	K	H	N	L	G	I	L	T	K	R	S	N	F	T>				
-----I-Ad α -1 DOMAIN-----																			
1060 *		1070 *		1080 *		1090 *		1100 *											
CCA	GCT	ACC	AAT	GAG	GCT	CCT	CAA	GCG	ACT	GTG	TTC	CCC	AAG	TCC	CCT				
GGT	CGA	TGG	TTA	CTC	CGA	CGA	GTT	CGC	TGA	CAC	AAG	GGG	TTC	AGG	GGA				
P	A	T	N	E	A	P	Q	A	T	V	F	P	K	S	P>				
-----><-----I-Ad α -2 DOMAIN-----																			
1110 *		1120 *		1130 *		1140 *		1150 *											
GTG	CTG	CTG	GGT	CAG	CCC	AAC	ACC	CTT	ATC	TGC	TTT	GTG	GAC	AAC	ATC				
CAC	GAC	GAC	CCA	GTC	GGG	TTG	TGG	GAA	TAG	ACG	AAA	CAC	CTG	TTG	TAG				
V	L	L	G	Q	P	N	T	L	I	C	F	V	D	N	I>				

FIG. 29D